

REMARKS

This amendment to the specification adds no new matter. Tables IV, V, and XIX, XX, XXII-XXIV, and XXVI-XXXII have been amended to include SEQ ID NOs. Substitute Sheets with a 1-inch margin at the left side are provided for Tables VII-XVIII. Applicants note that any changes in the number of pages of a Table is due to re-formatting to add the SEQ ID NOs.

The Table number on page 153 was amended to correct "XV" to "XIV". The amendment corrects a typographical error. The title of the table corresponds to Table XIV and therefore indicates that the page is properly designated as a Table XIV page.

This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-4570, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

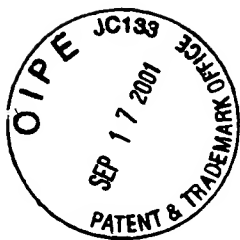
The information contained in the computer readable disk was prepared through the use of the software program "FastSEQ" and is identical to that of the paper copy.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,


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PATENT

APPENDIX A

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Amendment to the paragraph at page 51, lines 1-9:

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in the majority of the population. This can be accomplished by selecting amino acid sequences that bind to many, most, or all of the HLA class II molecules. These are known as "loosely HLA-restricted" or "promiscuous" T helper sequences. Examples of amino acid sequences that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; SEQ ID NO:4223), *Plasmodium falciparum* CS protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; SEQ ID NO:4224), and Streptococcus 18kD protein at positions 116 (GAVDSILGGVATYGAA; SEQ ID NO:4225). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Amendment to the paragraph at page 51, lines 10-20:

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.,* PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.,* PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVWANTLKAAa (SEQ ID NO:4226), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

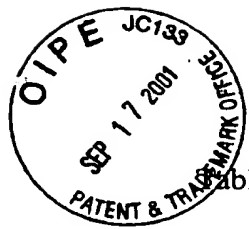


Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	4188	25
A*0201	941.01	FLPSDYFPSV	4189	5.0
A*0202	941.01	FLPSDYFPSV	4190	4.3
A*0203	941.01	FLPSDYFPSV	4191	10
A*0205	941.01	FLPSDYFPSV	4192	4.3
A*0206	941.01	FLPSDYFPSV	4193	3.7
A*0207	941.01	FLPSDYFPSV	4194	23
A*6802	1072.34	YVIKVSARV	4195	8.0
A*0301	941.12	KVFPYALINK	4196	11
A*1101	940.06	AVDLYHFLK	4197	6.0
A*3101	941.12	KVFPYALINK	4198	18
A*3301	1083.02	STLPETYVRR	4199	29
A*6801	941.12	KVFPYALINK	4200	8.0
A*2402	979.02	AYIDNYNKF	4201	12
B*0702	1075.23	APRTLVL	4202	5.5
B*3501	1021.05	FPFKYAAAF	4203	7.2
B51	1021.05	FPFKYAAAF	4204	5.5
B*5301	1021.05	FPFKYAAAF	4205	9.3
B*5401	1021.05	FPFKYAAAF	4206	10

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added

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	4207	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	4208	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	4209	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	4210	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	4211	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	4212	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	4213	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	4214	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	4215	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	4216	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	4217	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	4218	3.5
DRB1*1501	DR2w2 β 1	507.02	GRTQDENPVVHFFKNI VTPRTPPP	4219	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	4220	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	4221	58
DRB5*0101	DR2w2 β 2	553.01	QYIKANSKFIGITE	4222	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

added

HER2/NEU A01 Supermotif Peptides with Binding Data

Table VII

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
PTNASLSF	66	8		1
VTYNTDTF	272	8		2
GTYYKGIW	732	8		3
FTHQSDVW	899	8		4
VTACPYNV	296	8	0.1000	5
MTFGAKPY	916	8	-0.0021	6
PTAENPEY	1241	8	0.0030	7
TILWKDIF	166	8		8
KIFGSLAF	369	8		9
DIQEVQGY	76	8		10
RILHNGAY	434	8		11
QIAKGMSY	828	8		12
PICTIDVY	945	8	-0.0021	13
SLPDLSVF	418	8		14
YLVPOQGF	1023	8		15
ELAALCRW	2	8		16
DLSYMPIW	607	8		17
TLEEITGY	402	8	-0.0021	18
DLVDAEEY	1016	8		19
IVRGTOIF	101	8		20
TVPWDQLF	479	8		21
VVLGVVVF	664	8		22
KVLGSGAF	724	8		23
TVWELMTF	911	8		24
LVPQQGFF	1024	8		25
VVKDVFVF	1180	8		26
GVKPDLSY	603	8		27
LVTLMPY	796	8		28
YMIMVKCW	952	8		29
TSANIQEF	357	8		30
ESILRRRF	892	8		31
DSECRPRF	962	8		32
ASPLDSTF	997	8		33
GSQDLLNW	818	8		34
WSYGVTVW	906	8		35
DTILWKDIF	165	9		36
VTSANIQEF	356	9		37
HTVPWDQLF	478	9		38
VTWVWELMTF	910	9	0.1800	39
GTOLFEDNY	104	9	0.0430	40
ETLEEITGY	401	9	0.1300	41
LTCSPQPEY	1131	9		42
RIVRGTOIF	100	9		43
SLAFLPEF	373	9		44
YLVPOQGFF	1023	9		45
TLOGLGISW	444	9		46
QLCARGHCW	513	9		47

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Table VII
HER2/NEU A01 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
HLDMLRHL	42	9	9.1000	48
VLQGLPREY	546	9	0.0050	49
QLVTQLMPY	795	9	0.0024	50
LLDIDET	869	9	7.6000	51
PLPSETDGY	1119	9	0.0017	52
LVYNTDTF	271	9		53
LVVVLGVF	663	9		54
GVVKDFEAF	1179	9		55
CVTACPYN	295	9	0.0042	56
RMARDPQRF	978	9		57
PMCKGSRW	197	9		58
SMPNPEGRY	281	9	0.0028	59
VMAGVGSPY	773	9	0.0400	60
LMTFGAKPY	915	9	0.0011	61
DSLPLDSVF	417	9		62
LSYMPIWKF	608	9		63
ASCVTACPY	293	9	0.0550	64
GSGAFGT	727	9	0.0011	65
ASPLDSTF	997	9	0.0290	66
FSPAFDNL	1213	9	0.0430	67
PTQCVNCSQF	525	10		68
ITGYLYSAW	406	10		69
LTLOGLISW	443	10		70
FTQSDVWSY	899	10	2.7000	71
GTPTAENPEY	1239	10	0.0630	72
LHHNTHLCF	467	10		73
MIDSECRPF	960	10		74
LIQRNPQLCY	154	10	0.0300	75
YLPTNASLSE	64	10		76
ALVTYNTDTF	270	10		77
PLQEQLOVF	391	10		78
DLSPMPWKF	607	10		79
LLVVVLGVF	662	10		80
ALESILRRRF	890	10		81
QLCYQDTILW	160	10		82
HLCFVHTVPW	473	10		83
RLGSQDLN	816	10		84
ELHCPALVTY	265	10	0.0015	85
TLEETGYLY	402	10	1.1000	86
RLDIDET	868	10	1.3000	87
ELMTFGAKPY	914	10	0.0082	88
PLTCSPOPEY	1130	10	0.0072	89
AVTSANIQEF	355	10		90
KVKVLGSGAF	722	10		91
GVTWVELMTF	909	10		92
DVWSYGVTVW	904	10		93
DVYMIMVKCW	950	10		94

Table VII
HER2/NEU A01 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
VVOQNLELY	55	10	0.0180	95
RVLQGLPREY	545	10	0.0015	96
YVMAQVGSPY	772	10	1.1000	97
CMQIAKGMSY	826	10	0.3000	98
HSDCLACLHF	249	10		99
GSLAFLPESF	372	10		100
PSEGAGSDVF	1077	10		101
ESMPNPEGRY	280	10	0.1800	102
CSKPCARVCY	334	10	0.0016	103
PSGVKPDLSY	601	10	0.0010	104
FSPAFDNLYY	1213	10	5.5000	105
ETHLDMRLHLY	40	11	0.2800	106
ETLEETGYLY	401	11	0.4400	107
PTHDPSPLOQY	1102	11	0.0160	108
ETGYLYISAW	405	11		109
RLRVRGTQLF	98	11		110
ALIHNNHLCF	466	11		111
ILLVVVLGVWF	661	11		112
SLTLQGLGISW	442	11		113
FLQDIQEVQGY	73	11		114
VLIQRNPQLCY	153	11		115
VLSGAGFGTVY	725	11		116
FVHTVPWDOLF	476	11		117
QVYQGNLELY	54	11		118
TVQLVTQLMPY	793	11		119
TVPLPSETDGY	1117	11		120
SMPNPEGRYTF	281	11		121
WMIDSECRPRF	959	11		122
DMGDLVDAEEY	1013	11	0.0027	123
KSPNHVKITDF	854	11		124
FSRMARDPQRF	976	11		125
CSPMCKGSRGW	195	11		126
FSPAFDNLYYW	1213	11		127
ASCVTACPYNV	293	11	0.1900	128

Table VIII
HER2/NEU A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
AAKGLQSL	1094	8						129
AAKGLQSLPT	1094	10						130
AALCRWGL	4	8						131
AALCRWGLL	4	9						132
AALCRWGLLL	4	10	0.0010					133
AALCRWGLLLA	4	11						134
AAPOHPHPPA	1203	10						135
AARPAGAT	1159	8	0.0001					136
AARPAGATL	1159	9						137
AASTQVCT	20	8						138
AASTQVCTGT	20	10						139
AIKVLRENT	751	9						140
ALAVLDNGDPL	113	11						141
ALCRWGLL	5	8						142
ALCRWGLLL	5	9	0.0310					143
ALCRWGLLLA	5	10	0.0360	0.0022	0.8600	0.0019	0.0160	144
ALCRWGLLLAL	5	11						145
ALCSILRRRFT	890	11						146
ALIHNTHL	466	9	0.0210					147
ALLPGAA	14	8						148
ALLPGAAST	14	10						149
ALVTYNTDT	270	9	0.0001					150
AMPNQAQM	705	8	0.0001					151
AMPNQAQMRI	705	10	0.0007					152
AMPNQAQMRL	705	11						153
AQMRILKET	710	9						154
AQMRILKETEL	710	11						155
ATLERPKT	1165	8						156
ATLERPKTL	1165	9						157
AVENPEYL	1190	8						158
AVENPEYLT	1190	9						159
AVLDNGDPL	115	9	0.0004					160
AVTSANIQEFA	355	11						161
AVGILLV	657	8						162
AVGILLVV	657	9	0.0007					163
AVGILLVVV	657	10	0.0002					164
AVGILLVVVL	657	11						165
CAHYKDPFECV	587	11						166
CARCKGPL	224	8						167
CARCKGPLPT	224	10						168
CARVCYGL	338	8						169
CARVCYGLGM	338	10	0.0011					170
CLHFNHSGI	255	9						171
CLTSTVQL	789	8						172
CLTSTVQLV	789	9	0.0340					173
CLTSTVQLVT	789	10						174


Table VIII
HER2/NEU A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
CMQIAKGM	826	8						175
CMQIAKGMSTL	826	11						176
CQPCPINCT	623	9						177
CQPONGSV	567	8						178
CQPONGSVT	567	9						179
COSLTRTV	212	8						180
COSLTRTVCA	212	10						181
CQVYQGNL	53	8						182
CQVYQGNLEL	53	10						183
CQVYQGNLELT	53	11						184
CTGPKHSDCL	244	10						185
CTGPKHSDCLA	244	11						186
CTGTDML	26	8						187
CTGTDMLRL	26	10						188
CTHSCVDL	630	8						189
CTIDVYMI	947	8						190
CTIDVYMIM	947	9						191
CTIDVYMIMV	947	10						192
CVARCPGVS	596	9	0.0004					193
CVDLDDKGCPSA	634	11						194
CVEECRVL	540	8						195
CVEECRVLQGL	540	11						196
CVGEGACHQL	504	11						197
CVNCSQFL	528	8						198
CVTACPNYL	295	10	0.0001					199
DIDETETHA	871	9	0.0002					200
DIFHKNNQL	171	9						201
DIFHKNNQLA	171	10						202
DIFHKNNQLAL	171	11						203
DIQEVQGYV	76	9	0.0001					204
DIQEVQGYVL	76	10	0.0001					205
DIQEVQGYVLI	76	11						206
DLAARNVL	845	8						207
DLAARNVLV	845	9	0.0002					208
DLDDKGCPSA	636	9						209
DLGMAAKGL	1089	10	0.0001					210
DLGPASPL	993	8						211
DLGPASPLDST	993	11						212
DLEKGERL	933	9	0.0002					213
DLLNWCMI	821	9	0.0002					214
DLLNWCMIQA	821	10						215
DLVVFQNL	421	8	0.0003					216
DLVVFQNLQV	421	10						217
DLVVFQNLQVI	421	11	0.0002					218
DLVDAEEYL	1016	9	0.0002					219
DLVDAEEYLV	1016	10	0.0002					220

Table VIII
HER2/NEU A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
DMGDLVDA	1013	8						221
DMKLRLPA	30	8						222
DQDPPERGA	1224	9						223
DQLFRNPHQA	483	10						224
DQLFRNPHQAL	483	11						225
DTILWKDI	165	8						226
DVFAFGGA	1183	8						227
DVFAFGGAV	1183	9	0.0002					228
DVFDGDLGM	1084	9						229
DVFDGDLGMGA	1084	11						230
DVGSCTLV	307	8						231
DVGSCTLVCPPL	307	11						232
DVRLVHRDL	838	9	0.0002					233
DVRLVHRDLA	838	10						234
DVRLVHRDLAA	838	11						235
DVWSYGV	904	8						236
DVWSYGVTV	904	9	0.0002					237
DVYMIMVKCWM	950	11						238
EADQCACA	580	9						239
EAPRSLA	1069	8						240
EAYVMAGV	770	8						241
EILDEAYV	766	8						242
EILDEAYVM	766	9						243
EILDEAYVMA	766	10						244
EILKGGVL	147	8						245
EILKGGVLI	147	9						246
EITGYLYI	405	8	0.0001					247
EITGYLYISA	405	10						248
ELAALCRWGL	2	10	0.0001					249
ELAALCRWGILL	2	11						250
ELGSLAL	460	8						251
ELGSLALI	460	9	0.0004					252
ELHCPALV	265	8						253
ELHCPALVT	265	9						254
ELQRSLT	139	8						255
ELQRSLTEI	139	10						256
ELQRSLTEIL	139	11						257
ELRKVKVL	719	8						258
ELTYLPTNA	61	9						259
ELTYLPTNASL	61	11						260
ELVEPLTPSCA	695	11						261
ELVSEFSRM	971	9	0.0001					262
ELVSEFSRMA	971	10	0.0001					263
EQCAAGCT	238	8						264
EQLOVFET	395	8						265
EQLOVFETL	395	9						266

Table VIII
HER2/NEU A02 Supermotif with Binding Data



Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
EORASPLT	645	8						267
EORASPLTSI	645	10						268
EORASPLTSII	645	11						269
ETDGYVAPL	1123	9						270
ETDGYVAPLT	1123	10						271
ETELRKVKV	717	9						272
ETELRKVKVL	717	10						273
ETELVEPL	693	8						274
ETELVEPLT	693	9						275
ETEHADGGKV	874	11						276
ETHLDMLRHL	40	10						277
ETLEETGYL	401	10						278
EVQGYVLI	79	8						279
EVQGYVLI	79	9						280
EVRAVTS	352	8						281
EVRAVTSANI	352	10						282
EVTAE DGT	321	8						283
FAGCKKIFGSL	364	11						284
FLPESFDG DPA	376	11						285
FLQDIQEV	73	8						286
FLRQECV	534	8						287
FQNLQVIRGRI	425	11						288
FVHTVPWDQL	476	10	0.0001					289
FVVIQNE DL	986	9	0.0002					290
FVVIQNE DL	1093	9	0.0001					291
GAAGLQSL	1093	11						292
GAAGLQSLPT	1202	11						293
GAAPQPHPPA	19	9						294
GAASTQVCT	19	11						295
GAASTQVCTGT	19	11						296
GACQCP	621	8						297
GACQCPINCT	621	11						298
GAFGTVYKGI	729	10	0.0001					299
GAGSDVFDGDL	1080	11						300
GAKPYDGI	919	8						301
GAKPYDGI	919	10	0.0002					302
GAMPNQAQM	704	9						303
GAMPNQAQMRI	704	11						304
GAPPSTFKGT	1231	10	0.0001					305
GASPGGLREL	131	10						306
GATLERPKT	1164	9	0.0002					307
GATLERPKTL	1164	10	0.0002					308
GAVENPEYL	1189	9	0.0002					309
GAVENPEYLT	1189	10	0.0030					310
GAYSLTLQGL	439	10	0.0005					311
GICELHCPA	262	9						312
GICELHCPAL	262	10						

Table VIII
HER2/NEU A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
GICELHCPALV	262	11						313
GICLTSTV	787	8						314
GICLTSTVQL	787	10	0.0004					315
GICLTSTVQLV	787	11						316
GLIKRRQOKI	672	11						317
GILLVVVL	660	8						318
GILLVVVLGV	660	10	0.0007					319
GILLVVVLGVV	660	11						320
GIPAREIPDL	925	10	0.0001					321
GIPAREIPDLL	925	11						322
GISWLGRLSL	449	10	0.0003					323
GIWPDGENV	737	10	0.0002					324
GLACHQLCA	508	9	0.0120			0.0001	0.0044	325
GLALIHNT	464	9			0.0790			326
GLALIHNTHL	464	11						327
GLARLLDI	865	8						328
GLARLLDIDET	865	11						329
GLEPSEEEA	1062	9	0.0018					330
GLGISWLG	447	9	0.0017					331
GLGMEHLREV	344	10						332
GLLLALLPPGA	10	11						333
GLPREYVNA	549	9						334
GLRELQLRSL	136	10	0.0001					335
GLRELQLRSLT	136	11						336
GLRSLREL	454	8						337
GMEHLREV	346	8						338
GMEHLREVRA	346	10						339
GMEHLREVRAV	346	11						340
GMGAAGKL	1091	8						341
GMGAAGLQSL	1091	11						342
GMSYLEDV	832	8						343
GMSYLEDVRL	832	10	0.0017					344
GMSYLEDVRLV	832	11						345
GQECVEECRV	537	10						346
GQECVEECRVL	537	11						347
GTDMLRL	28	8						348
GTDMLRLPA	28	10						349
GTPTAENPEYL	1239	11						350
GTQLFEDNYA	104	10						351
GTQLFEDNYAL	104	11						352
GTYYKGIWI	732	9						353
GVGSPYVSRL	776	10	0.0001					354
GVGSPYVSRL	776	11						355
GVKPDLSYM	603	9						356
GVKPDLSYMPI	603	11						357
GVLQRNPQL	152	10	0.0036					358

11
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Table VIII
HER2/NEU A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
GVTWELM	909	8						359
GVTWELMT	909	9						360
GVVFGIL	668	8						361
GVVKDVFA	1179	8						362
HADGKVP	878	9	0.0002					363
HLCFVHTV	473	8						364
HLDMLRHL	42	8						365
HLREVRV	349	8						366
HLREVRVVT	349	9						367
HLREVRVTS	349	11						368
HLYGCCV	48	8						369
HLYGCCV	48	9	0.0340					370
HQALLHTA	490	8						371
HQSDVWSYGV	901	10						372
HQSDVWSYGV	901	11						373
HTANRPEDEC	495	11						374
HTVPWDQL	478	8						375
HVKITDFGL	858	9	0.0002					376
HVKITDFGLA	858	10						377
HVRENRGRL	809	9	0.0002					378
IAHNQVRQV	86	9						379
IAHNQVRQVPL	86	11						380
IAKGMSTYL	829	8						381
IAKGMSTYLEDV	829	11						382
IISAVVGI	654	8						383
IISAVVGIL	654	9	0.0005					384
IISAVVGILL	654	10	0.0120					385
IISAVVGILLV	654	11						386
ILDEAYVM	767	8						387
ILDEAYVMA	767	9	0.0210	0.0001	0.0024	0.0012	0.0003	388
ILDEAYVMAGV	767	11						389
ILHNGAYSL	435	9	0.2100					390
ILHNGAYSLT	435	10						391
ILHNGAYSLTL	435	11						392
ILIKRRQKI	673	10						393
ILKETELRV	714	10						394
ILKGGVLI	148	8	0.0001					395
ILLVVVLGV	661	9	0.0020					396
ILLVVVLGVV	661	10	0.0006					397
IMVKCWM	954	8						398
IOEFAGCKKI	361	10						399
IOEVQGV	77	8						400
IOEVQGVY	77	9						401
IOEVQGVYLI	77	10						402
IOEVQGVYLI	77	11						403
IQNEDLGPA	989	9						404

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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
ITDFGLRL	861	9						405
ITDFGLARLL	861	10						406
ITGYLYISA	406	9						407
KANKEILDEA	762	10						408
KIFGSLAFL	369	9	0.1500					409
KIPVAIV	747	8						410
KIPVAIKVL	747	9	0.0002					411
KIRKYTMRRLL	681	10	0.0001					412
KIRKYTMRRLL	681	11						413
KITDFGLA	860	8						414
KITDFGLARL	860	10	0.0020					415
KITDFGLARLL	860	11						416
KLRLPASPET	32	10						417
KLSPKNGV	1171	10						418
KLSPKNGVV	1171	11						419
KVKVLGSA	722	9						420
KVLGSGAFGT	724	10						421
KVLGSGAFGT	724	11						422
KVLRNTSPKA	753	11						423
KVPIKWMA	883	8						424
KVPIKWMA	883	9	0.0002					425
LAALCRWGL	3	9						426
LAALCRWGLL	3	10	0.0022					427
LAALCRWGLLL	3	11						428
LAARNVLV	846	8						429
LACHQLCA	509	8						430
LACLFNHSIGI	253	11						431
LALIHNT	465	8						432
LALIHNTHL	465	10						433
LALLPPGA	13	8						434
LALLPPGAA	13	9						435
LALLPPGAAST	13	11						436
LALTIDT	179	8						437
LAPSEGAGSDV	1075	11						438
LARLLDIDET	866	10						439
LAVLDNGDPL	114	10	0.0002					440
LIAHNVQVQV	85	10	0.0001					441
LIDITNRSRA	183	9						442
LIIHNTHL	467	8						443
LIIHNTHLCFV	467	11						444
LIIKROOKI	674	9						445
LIIQNPQL	154	8						446
LLALLPPGA	12	9	0.0008					447
LLALLPPGAA	12	10	0.0006					448
LLDIDETEHYA	869	11						449
LLEDDDMGDL	1008	10	0.0001					450

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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
LLEDDDMGDLV	1008	11						451
LLEKGERL	934	8						452
LLGICLTST	785	9						453
LLGICLTSTV	785	10	0.0490					454
LLLALLPPGA	11	10	0.0034					455
LLLALLPPGAA	11	11						456
LLNWCMI	822	8						457
LLNWCMIQIA	822	9	0.0046					458
LLPPGAAS	15	9	0.0007					459
LLPPGAASSTQV	15	11						460
LLQETELV	690	8						461
LLQETELVEPL	690	11						462
LLVVLGV	662	8						463
LLVVLGVV	662	9						464
LMPYGCLL	800	8	0.0001					465
LMPYGCLLDHV	800	11						466
LQDQEVQGVV	74	11						467
LQETELVEPL	691	10						468
LQETELVEPLT	691	11						469
LQGLGISWL	445	9						470
LQGLGISWGL	445	11						471
LQGLPREYV	547	9						472
LQGLPREYVNA	547	11						473
LQRLSLTEI	140	9						474
LQRLSLTEIL	140	10						475
LOPEQLQV	392	8						476
LOPEQLQVFET	392	11						477
LQRLRIVRG	96	10						478
LQRYSEDPT	1109	9						479
LQRYSEDPTV	1109	10						480
LQVFETLEEI	397	10						481
LQVFETLEEIT	397	11						482
LQVIRGRI	428	8						483
LQVIRGRIL	428	9						484
LTCSPQPEYV	1131	10						485
LTELKGGV	145	9						486
LTELKGGVL	145	10						487
LTELKGGVLI	145	11						488
LTLDITNRSRA	181	11						489
LTLQGLGI	443	8						490
LTLQGLGISWL	443	11						491
LTPQGGAA	1197	8						492
LTPSGAMPNQA	700	11						493
LTRTVACGCCA	215	11						494
LTSISAV	651	8						495
LTSISAVV	651	9						496

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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
LTSISAVVGI	651	11						497
LTSTVQLV	790	8						498
LTSTVQLVT	790	9						499
LTSTVQLVTQL	790	11						500
LYLPTNA	62	8						501
LYLPTNASL	62	10						502
LYLPTNAEV	313	10						503
LVCPLHNEV	313	11	0.0002					504
LVCPLHNEVT	313	11						505
LVDAEEYL	1017	8						506
LVDAEEYLV	1017	9	0.0030					507
LVDAEEYLV	1017	9						508
LVEPLTPSGA	696	10						509
LVEPLTPSGAM	696	11						510
LVHRDLAA	841	8						511
LVHRDLAARNV	841	11						512
LKSPNHV	852	8						513
LKSPNHVKI	852	10						514
LKSPNHVKIT	852	11	0.0001					515
LVSEFSRM	972	8	0.0001					516
LVSEFSRMA	972	9						517
LVTLQMPYGC	796	11						518
LVTYNTDT	271	8						519
LVVVLGVV	663	8						520
LVVVLGVVFGI	663	11						521
MAGVGSPPV	774	9	0.0014					522
MARDPQRFV	979	9	0.0001					523
MARDPQRFVV	979	10						524
MARDPQRFVVI	979	11						525
MIMVKCWM	953	8	0.0051					526
MIMVKCWM	953	9						527
MLRHLVQGCQV	45	11						528
NQIAKGMSTL	827	10						529
MTFGAKPYDGI	916	11						530
MVHHRHRSST	1042	11						531
NASLSFLQDI	68	10	0.0001					532
NQEFAGCKKI	360	11						533
NLETLTPT	59	9						534
NLETLTPTNA	59	11						535
NLQVIRGRI	427	9						536
NLQVIRGRIL	427	10	0.0001					537
NQAQMRIL	708	8						538
NQAQMRILKET	708	11						539
NQEVTAEDGT	319	10						540
NQLALTLI	177	8						541
NQLALTLIDT	177	10						542
NQVRQVPL	89	8						
NQVRQVPLQRL	89	11						

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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
NTAPLQPEQL	388	10						543
NTDIFESM	275	8						544
NTHLCFVHT	471	9						545
NTHLCFVHTV	471	10						546
NTSPKANKEI	758	10						547
NTSPKANKEIL	758	11						548
NTTPVTGA	125	8						549
NVKIPVAI	745	8						550
NVKIPVAIKV	745	10	0.0001					551
NVKIPVAIKVL	745	11						552
NVLKSPNHV	850	10	0.0001					553
PAARPAGA	1158	8						554
PAARPAGAT	1158	9						555
PAARPAGATL	1158	10	0.0001					556
PAEQRASPL	643	9	0.0001					557
PAEQRASPLT	643	10	0.0001					558
PAFSPAFDNL	1211	10	0.0001					559
PAGATLERPKT	1162	11						560
PALVTYNT	269	8						561
PALVTYNTDT	269	10						562
PAPGAGGM	1035	8						563
PAPGAGGMV	1035	9						564
PAREIPDL	927	8						565
PAREIPDLL	927	9	0.0001					566
PASNTAPL	385	8						567
PASPETHL	36	8						568
PASPETHLDM	36	10	0.0001					569
PASPETHLDMML	36	11						570
PASPLDST	996	8						571
PICTIDVYM	945	9						572
PICTIDVYMI	945	10						573
PICTIDVYMIM	945	11						574
PIKWMALESIL	885	10						575
PIKWMALESIL	885	11						576
PINCTHSCV	627	9	0.0002					577
PINCTHSCVDL	627	11						578
PIWKFDEEGA	612	11						579
PLAPSEGA	1074	8						580
PLDSTFYRSL	999	10	0.0001					581
PLDSTFYRSL	999	11						582
PLNQEV	316	8						583
PLNQEVTA	316	9						584
PLNNTTPV	122	8						585
PLNNTTPVT	122	9						586
PLNNTTPVTGA	122	11						587
PLPAARPA	1156	8						588

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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
PLPAARPAGA	1156	10						589
PLPAARPAGAT	1156	11						590
PLPSETDGYV	1119	10	0.0001					591
PLPSETDGYVA	1119	11						592
PLPSETDGYVA	391	9	0.0002					593
PLQPEQLQV	95	8						594
PLQRLRIV	95	11						595
PLQRLRIVRGT	95	11						596
PLQRYSEDPT	1108	10						597
PLQRYSEDPTV	1108	11						598
PLTCSQPPEYV	1130	11						599
PLTPSGAM	699	8						600
PLTSIISA	650	8						601
PLTSIISAV	650	9	0.0015					602
PLTSIISAVV	650	10	0.0003					603
POLCYQDT	159	8						604
POLCYQDTI	159	9						605
POLCYQDTIL	159	10						606
PQPEYVNPDPV	1135	11						607
PQHPPPA	1205	8						608
PQPICTI	942	8						609
PQPICTIDV	942	10						610
POPSPREGPL	1147	11						611
PQQGFCPDPA	1026	11						612
PTAENPEYL	1241	9						613
PTAENPEYLG	1241	11						614
PTDCCHEQCA	232	10						615
PTDCCHEQCAA	232	11						616
PTHDPSP	1102	8						617
PTNASLSFL	66	9						618
PTQVNCQSFL	525	11						619
PTVPLPSET	1116	9						620
PVAIKVIRENT	749	11	0.0001					621
PVTGASPGGL	128	10						622
QAQMRILKET	709	10	0.0006					623
QIAKGMMSYL	828	9						624
QLALTLDIT	178	9						625
QLCYQDTI	160	8						626
QLCYQDTIL	160	9						627
QLFEDNYA	106	8						628
QLFEDNYAL	106	9	0.4600					629
QLFEDNYALA	106	10	0.0140				0.5400	630
QLFEDNYALAV	106	11		0.0065	1.1000	0.0170		631
QLFRNPHQA	484	9	0.0062					632
QLFRNPHQAL	484	10	0.0003					633
QLFRNPHQALL	484	11						634
QLMPYGC	799	8						

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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
QLMPYGCLL	799	9	0.0230	0.0044	0.0880	0.0052	0.0031	635
QLQVFETL	396	8						636
QLQVFETLEEI	396	11						637
QLRSLTEI	141	8						638
QLRSLTEIL	141	9	0.0008					639
QMRILKET	711	8						640
QMRILKETEL	711	10	0.0001					641
QQGFFCPDPA	1027	10						642
QQKIRKYT	679	8						643
QQKIRKYTM	679	9						644
QVCTGTDM	24	8						645
QVCTGTDMKL	24	10	0.0001					646
QVFETLEEI	398	9						647
QVFETLEEIT	398	10						648
QVIRGRIL	429	8						649
QVPLQRLRI	93	9						650
QVPLQRLRIV	93	10	0.0001					651
QVRQVPLQRL	90	10	0.0001					652
QVVGQNLLEL	54	9	0.0001					653
QVVGQNLLELT	54	10						654
RACHPCSPM	190	9	0.0001					655
RASPLTSI	647	8						656
RASPLTSII	647	9	0.0002					657
RASPLTSIISA	647	11						658
RAVTSANI	354	8						659
RIHNGAYSL	434	10	0.0180					660
RIHNGAYSLT	434	11						661
RIKTEL	713	8						662
RILKETELRKV	713	11						663
RIVRGTQL	100	8						664
RLGSQDLL	816	8						665
RLLDIDET	868	8						666
RLIGICLT	784	8						667
RLIGICLTST	784	10						668
RLIGICLTSTV	784	11						669
RLLOETEL	689	8						670
RLLOETELV	689	9	0.0910					671
RLPASPET	34	8						672
RLPASPETHL	34	10	0.0001					673
RLPQPICT	940	9	0.0002					674
RLPQPICTI	940	10						675
RLRIVRG	98	8						676
RLRIVRGTL	98	10	0.0001					677
RLVHRDLA	840	8						678
RLVHRDLAA	840	9	0.0001					679
RMARDPQRFV	978	10	0.0020					680


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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
RMARDPQRFVV	978	11						681
ROQIRKYYT	678	9						682
ROQIRKYYTM	678	10						683
QVPLQRL	92	8						684
QVPLQRLRI	92	10						685
QVPLQRLRIV	92	11						686
RTVCAGGCA	217	9						687
RVCYGLGM	340	8						688
RVCYGLGMEHL	340	11						689
RVLQGLPREYV	545	11						690
SANIQEFA	358	8						691
SAVVGILL	656	8						692
SAVVGILLV	656	9	0.0009					693
SAVVGILLVV	656	10						694
SAVVGILLVVV	656	11						695
SAWPDSLPL	413	10						696
SIISAVVGI	653	9	0.0002	0.0082	0.2900	0.0130	0.2700	697
SIISAVVGIL	653	10	0.0720					698
SIISAVVGILL	653	11	0.0002					699
SILRRRT	893	8						700
SILEDDDM	1007	8						701
SLEDDDMGDL	1007	11						702
SLPDLVSFQNL	418	11						703
SLPTHDPSP	1100	10	0.0039					704
SLRELGSGL	457	9	0.0002					705
SLRELGSGLA	457	10						706
SLRELGSGLAL	457	11						707
SLSFLQDI	70	8						708
SLSFLQDIEV	70	11						709
SLTEILKGGV	144	10	0.0150					710
SLTEILKGGVL	144	11						711
SLTLQGLGI	442	9	0.0003					712
SLTRTVCA	214	8						713
SMNPPEGRYT	281	10						714
SQDLLNWCM	819	9						715
SQDLLNWCMI	819	11						716
SQFLRGQECV	532	10						717
STDVGSCT	305	8						718
STDVGSCTL	305	9						719
STDVGSCTLV	305	10	0.0001					720
STFKGTPT	1235	8						721
STFKGTPTA	1235	9						722
STFYRSL	1002	8						723
STOVCTGT	22	8						724
STOVCTGTDM	22	10						725
STRSGGGDL	1051	9						726

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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
STRSGGDLT	1051	10						727
STRSGGDLTL	1051	11						728
STVQLVTQL	792	9						729
STVQLVTQLM	792	10						730
SVFQNLQV	423	8						731
SVFQNLQVI	423	9	0.0017					732
SVTCFGPEA	573	9						733
TACPYNYL	297	8						734
TACPYNYLST	297	10						735
TAENPEYL	1242	8						736
TAENPEYGL	1242	10	0.0001					737
TANRPEDEC	496	10						738
TAPLQPEQL	389	9	0.0002					739
TAPLQPEQLQV	389	11						740
TIDVYMIM	948	8						741
TIDVYMIMV	948	9	0.0005					742
TLEEITGYL	402	9	0.0018					743
TLEEITGYLYI	402	11						744
TLERPKTL	1166	8						745
TLGLEPSEEA	1060	11						746
TLIDTNRSA	182	10						747
TLQGLGISWL	444	10						748
TLSPKNGV	1172	9	0.0011					749
TLSPKNGVV	1172	10	0.0002					750
TLVCPHNEV	312	11	0.0001					751
TMRRLLQET	686	9						752
TMRRLLQETEL	686	11						753
TOCVNCSQFL	526	10						754
TQLFEDNYA	105	9						755
TQLFEDNYALA	105	10						756
TQLFEDNYAL	105	11						757
TQLMPYGCL	798	9						758
TQLMPYGCLL	798	10						759
TQVCTGTD	23	9						760
TQVCTGTDML	23	11						761
TVCAGGCA	218	8						762
TVPLPSET	1117	8						763
TVQLVTQL	793	8						764
TVQLVTQLM	793	9						765
TVWELMTFGA	911	10						766
TVYKGIWI	733	8						767
VAIKVLRENT	750	10						768
VARCPGV	597	8						769
VIONEDLGA	988	10						770
VIRGRILHNGA	430	11						771
VLDNGDPL	116	8						772

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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
VLDNGDPLNNT	116	11						773
VLGSGAFGT	725	9						774
VLGSGAFGT	725	10	0.0007					775
VLGVVFGI	666	8						776
VLGVVFGIL	666	9	0.0005					777
VLGVVFGILI	666	10						778
VLIHNOV	84	8						779
VLIHNOVRQV	84	11						780
VLIQNPQL	153	9	0.0290					781
VLQGLPREYV	546	10	0.0009					782
VLRENTSPA	754	10						783
VLVKSPNHV	851	9	0.0002					784
VLVKSPNHVKI	851	11						785
VMAVGSPYV	773	10	0.0180					786
VQGNLELT	56	8						787
VQGNLELYL	56	10						788
VQGYLIA	80	8						789
VQLVTQLM	794	8						790
VTACPNYL	296	9						791
VTACPNYVLT	296	11						792
VTCFGEA	574	8						793
VTGASPGGL	129	9						794
VTQLMPYGCL	797	10						795
VTQLMPYGCLL	797	11						796
VTSANIQEFA	356	10						797
VTWELMT	910	8						798
VTWELMTFGA	910	11						799
VTYNTDTFESM	272	11						800
WGILLV	658	8						801
WGILLVV	658	9	0.0005					802
WGILLVVVL	658	10	0.0009					803
WQINEDL	987	8						804
WQINEDLGPA	987	11						805
WKDVFVAFGGA	1180	11						806
VLGVVFGI	665	9	0.3500	0.0001	0.0040	0.0086	0.0200	807
VLGVVFGIL	665	10	0.0027					808
VLGVVFGILI	665	11						809
VQGNLEL	55	8						810
VQGNLELT	55	9						811
VQGNLELYL	55	11						812
VVLGVVFGI	664	10	0.0032					813
VVLGVVFGIL	664	11						814
WIPDGENV	739	8						815
WIPDGENVKI	739	10						816
WLGRLREL	452	10	0.0001					817
WMALESIL	888	8						818

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Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
YISAWPDSL	411	9	0.0003					819
YLEDVRLV	835	8						820
YGLDVPV	1248	8						821
YLPINASL	64	8						822
YLPINASLSFL	64	11						823
YLSTDVGSCT	303	10						824
YLSTDVGSCTL	303	11	0.0002					825
YLTPOGGA	1196	8						826
YLTPOGGAA	1196	9	0.0001					827
YLYSAWPDLSL	409	11						828
YIMVVKCWM	952	9	0.0230	0.0001	0.0160	0.0014	0.0400	829
YIMVVKCWM	952	10	0.0600	0.0004	0.0300	0.0190	0.0011	830
YQDTLWKDI	163	10						831
YQGCQVVGNI	50	11						832
YTFGASCV	289	8						833
YTFGASCVT	289	9						834
YTFGASCVTA	289	10						835
YTMRLLOET	685	10						836
YVLIHNOV	83	9						837
YVMAGVGSPYV	772	11	0.0005					838
YVNAHCL	554	8						839
YVSRLLGI	781	8						840
YVSRLLGICL	781	10	0.0004					841
YVSRLLGICLT	781	11						842

Table IX
HER2/NEU A03 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO.
AAGCTGPK	241	8						843
AARNVLVK	847	8						844
AARPAGATLER	1159	11						845
ALESILRR	890	8	0.0013	0.0006				846
ALESILRRR	890	9						847
ALLHTANR	492	8	0.0004	0.0005				848
ALLTIDTNR	180	9						849
ALLTIDTNR	180	11						850
ALTLDITNRSR	180	11	0.0004	0.0006				851
AMPNQAQMR	705	9						852
ASPETHLDMLR	37	11						853
ASPLDSTFYR	997	10	0.0003	0.0670	0.1200	0.0140	0.0520	854
CAAGCTGPK	240	9	0.0021	0.0021				855
CAGOCARCK	220	9	-0.0002	-0.0002				856
CLLDHVRENK	805	10	0.0003	0.0001				857
CSPMCKGSR	195	9	-0.0008	-0.0001				858
CTGTDMKLR	26	9	0.0002	0.0005				859
CTHSCVDLDDK	630	11						860
CTIDVYMIMVK	947	11						861
CVACAHYK	584	8						862
CVARCPGSK	596	10	0.0020	0.0042	0.0008	0.0064	0.0093	863
CVNCSQFLR	528	9	0.0015	0.0310	0.5300	0.5800	0.4400	864
DLAARNVLVK	845	10	0.0018	0.0007				865
DLMGGAKE	1089	8						866
DLEKGER	933	8						867
DLNWCNQIAK	821	11						868
DLSYMPIWK	607	9	0.0005	0.0100	0.0002	0.0880	0.0310	869
DSECRPRFR	962	9	-0.0002	-0.0002				870
DTILWKDIFHK	165	11						871
DVRPPSPSR	1144	10	0.0003	0.0001				872
DVYMIMVK	950	8						873
EILKGGVLIQR	147	11						874
EIPDLLEK	930	8						875
EIPDLLEKGER	930	11						876
ELMTFGAK	914	8						877
ELYSEFSR	971	8						878
ELVSEFSRMAR	971	11	0.0003	-0.0002				879
ESMPNPEGR	280	9						880
ESSEDCQSLTR	207	11						881
ETELRKVK	717	8	0.0003	0.0001				882
ETEHADGKG	874	10						883
ETHLDMLR	40	8						884
EVTAEADGTQR	321	10	0.0002	0.0001				885
FSRMARDPQR	976	10	-0.0002	0.0010				886
GAGFTVYK	729	8	-0.0002	0.0043				887
GAGGMVHHR	1038	9						888
GAGGMVHHRH	1038	11						889
GAKPYDGIPAR	919	11						

Table IX
HER2/NEU A03 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO.
GAMPNOAQMRR	704	10	-0.0002	0.0041				890
GAPPSTFK	1231	8						891
GASPGGLR	131	8						892
GATLERPK	1164	8						893
GLIKRRQOK	672	8	0.0150	0.0014				894
GISWLGLR	449	8						895
GISWLGLRSLR	449	11						896
GIWPDGENVK	737	11						897
GLACHQLCAR	508	10	0.0110	0.0001				898
GLEPSEEEAPR	1062	11						899
GLISWLGLR	447	10	0.0037	0.0001				900
GLGMEHLR	344	8						901
GLGMEHLREVR	344	11	0.0002	0.0003				902
GLPREYVNAR	549	10						903
GLRELQLR	136	8	-0.0002	-0.0002				904
GMEHLREVR	346	9	-0.0002	0.0002				905
GMSYLEDVR	832	9						906
GMVHHRHR	1041	8						907
GSAGFTVYK	727	10	0.0660	0.1300	0.0014	-0.0013	0.0012	908
GTORCEKCSK	327	10	0.0210	0.6100	0.0140	0.0012	0.0100	909
GVGSPYVSR	776	9	0.0010	0.0066	0.0019	0.0025	0.0011	910
GVVFGILIK	668	9	0.0047	0.0890	0.0019	0.0025	0.0011	911
GVVFGILIKR	668	10	0.0180	0.0330	0.0590	0.0140	0.4300	912
GVVFGILIKRR	668	11						913
HADGKVPK	878	10	0.0003	0.0008				914
HSCVDLDDK	632	9	-0.0002	0.0007				915
HTVPWDQLFR	478	10	0.0035	0.0720	0.9600	0.3300	2.0000	916
HKITDFGLAR	858	11						917
HYRENRR	809	8	0.3800	0.0097	0.0760	0.0064	0.0001	918
ILIKRRQOK	673	9						919
ILIKRRQOKIR	673	11						920
ILKETELR	714	8	0.0190	0.0023	0.0009	0.0010	0.0001	921
ILKETELRK	714	9						922
ILKETELRKVK	714	11						923
ILKGGVLQIR	148	10	0.0400	0.0005	0.7300	0.2400	0.0390	924
ILWKDIFHK	167	9	0.2800	0.3100	0.2200	0.0300	0.0046	925
ISWLGRLSLR	450	10	0.0410	0.0027	2.6000	0.1300	0.1100	926
ITDFGLAR	861	8						927
KIPVAIKVLR	747	10	0.0009	0.0099				928
KIRKYTMRR	681	8	0.0010	0.0004				929
KIRKYTMRR	681	9	0.7600	0.0018	1.1000	0.0072	0.0002	930
KITDFGLAR	860	9	0.1700	0.2400	0.1800	0.0012	0.0049	931
KVLRENTSPK	753	10	0.3800	0.2200	0.0068	0.0012	0.0008	932
LAARNVLVK	846	9	0.0580	0.0285	-0.0005	-0.0012	0.0160	933
LACHQLCAR	509	9	-0.0002	0.0003				934
LALTLDITNR	179	10	-0.0002	0.0003				935
LIAHNQVR	85	8						936

Table IX
HER2/NEU A03 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO.
LIDTNRSR	183	8						937
LIKRRQOK	674	8						938
LIKRRQOKIR	674	10	0.0002	0.0001				939
LIKRRQOKIRK	674	11						940
LLDHVREN	806	9	0.0370	0.0006	0.0360	0.0890	0.0014	941
LLDHVRENRR	806	11						942
LLNWCMIQAK	822	10	0.1400	0.1400	0.0100	0.0088	0.0086	943
LSPGKNGVVK	1173	10	-0.0002	0.0003				944
LSVFQNLQVIR	422	11						945
LSYMPIWK	608	8						946
LTLIDTNR	181	8						947
LTLIDTNRSR	181	10	0.0002	0.0005				948
LVHRDLAAR	841	9	0.0040	0.0014				949
LVKSPNHVK	852	9	0.4800	0.0700	0.0990	0.0370	0.1100	950
LYSEFSRMAR	972	10	0.0072	0.0330	0.3700	0.2300	0.2200	951
MAGVGSPYVSR	774	11						952
MALESILR	889	8						953
MALESILRR	889	9	0.0034	0.0237	0.0940	0.2200	0.0630	954
MALESILRRR	889	10	0.0011	0.0003				955
MIDSECRPR	960	9	0.0017	0.0006				956
MIDSECRPRFR	960	11						957
MSYLEDVR	833	8						958
NIQEFAGCK	360	9	0.0002	0.0036				959
NIQEFAGCKK	360	10	0.0003	0.0056				960
NLQVIRGR	427	8						961
NTSPKANK	758	8						962
NVKIPVAIK	745	9	0.0058	0.0007	0.0015	0.0820	0.1200	963
NVLKSPNHVK	850	11						964
PAGATLER	1162	8						965
PAGATLERPK	1162	10	-0.0002	-0.0002				966
PAKEIPDLLEK	927	11						967
PASPLDSTFYR	996	11						968
PLDSTFYR	999	8						969
PLQRLRIVR	95	9	0.0002	0.0001				970
PSEEEAPR	1065	8						971
PTHDPSPQR	1102	10	0.0003	0.0001				972
PVAIKVLR	749	8						973
PVTGASPGGLR	128	11	0.0046	0.0010				974
QALLHTANR	491	9						975
QAQMRILK	709	8						976
QALTLIDTNR	178	11						977
QLCYQDTILWK	160	11			0.0270	0.0047	0.0002	978
QLRSLTEILK	141	10	0.2000	0.0130				979
QMRILKETELR	711	11						980
QVCTGTDMK	24	9	0.0007	0.0520	0.0002	0.0006	0.0110	981
QVCTGTDMKLR	24	11						982
QVPLQLRL	93	8						983

Table IX
HER2/NEU A03 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO.
QVPLRLRIVR	93	11						984
QVROVPLQR	90	9	0.0029	0.0005				985
QVROVPLRLR	90	11						986
RACHPCSPMCK	190	11						987
RILKETELR	713	9	0.0007	0.0038				988
RILKETELRK	713	10	0.0570	0.1100	0.0055	0.0013	0.0002	989
RLVHRDLAAR	840	10	0.1800	0.0001	0.9500	0.0021	0.0036	990
RMARDPQR	978	8						991
RSLTEILK	143	8	0.0068	0.0130	0.4500	0.0220	0.0250	992
RTVCAGGCAR	217	10						993
RVLQLGLPR	545	8						994
SANIOEFAGCK	358	11						995
SMPNPEGR	281	8						996
SSEDCQSLTR	208	10	-0.0002	0.0020				997
STQVCTGTDNK	22	11	0.0170	0.0750	0.0340	0.0390	0.2500	998
SVFQNLQVIR	423	10						999
TAEDGTQR	323	8						1000
TAEDGTQRCEK	323	11						1001
TIDVYIMVVK	948	10	0.0130	0.1200	0.0018	0.0120	0.0250	1002
TILWKDFHK	166	10	0.0430	3.6000	0.0370	0.0420	0.0400	1003
TLIDTNRSR	182	9	0.0004	0.0005				1004
TLSPKNGVVK	1172	11		0.0230	0.1400	0.0890	0.0970	1005
TVCAGGCAR	218	9	0.0004					1006
TVCAGGCARCK	218	11	0.0006	0.0072				1007
TPWDQLFR	479	9						1008
TVWELMTFGAK	911	11	0.0100	-0.0002				1009
VARCPGVK	597	9						1010
VLGYVFGILIK	666	11	0.0033	0.0007				1011
VLIHNOVR	84	9	0.4000	0.0130	0.1400	0.1000	0.0001	1012
VLRENTSPK	754	9	0.0820	0.0072	0.0052	0.0032	0.0005	1013
VLKSPNHVK	851	10	-0.0002	0.0021				1014
VSEFSMAR	973	9	0.0002	0.0140	0.0011	0.0037	0.1000	1015
VTAEDGTQR	322	9	0.0002	0.0005				1016
VTGASPGGLR	129	10						1017
VVFGLIK	669	8						1018
VVFGLIKR	669	9	0.1100	0.7200	1.4000	0.3700	2.0000	1019
VVFGLIKRR	669	10	0.0030	0.0160	0.0620	0.1500	0.5400	1020
WIPDGENVK	739	9	0.0002	0.0001				1021
WLGRLSLR	452	8	-0.0002	-0.0002				1022
WMALESILR	888	10	0.0085	0.0016				1023
WMALESILRR	888	11						1024
WMALESILRRR	888	11						1025
WMIDSECR	959	8	-0.0002	0.0002				1026
WMIDSECRPR	959	10	0.0003	0.0001				1027
YLEDVRLVHR	835	10	0.0043	0.0013				1028
YVLIHNOVR	83	10						1029
YVNPQDVR	1139	8						1030

Table X
HER2/NEU A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
AFDNLYYW	1216	8	0.0039	1031
AFGAVENPEY	1186	11		1032
AFGTVYKGI	730	9	0.0002	1033
AFGTVYKGIW	730	10	0.0010	1034
AFGTVYKGIWI	730	11	0.0008	1035
AFSPAFDNL	1212	9	0.0011	1036
AFSPAFDNLY	1212	10		1037
AFSPAFDNLYY	1212	11		1038
ALAVLDNGDPL	1113	11		1039
ALCRWGLL	5	8		1040
ALCRWGLLL	5	9		1041
ALCRWGLLLL	5	11		1042
ALCSILRRRF	890	10		1043
ALIHNTHL	466	9		1044
ALIHNTHLCF	466	11		1045
ALVTYNTDTF	270	10		1046
AMPNQAQM	705	8		1047
AMPNQAQMRI	705	10	0.0002	1048
AMPNQAQMRIL	705	11	-0.0003	1049
ATLERPKTL	1165	9		1050
AVENPEYL	1190	8		1051
AVLDNGDPL	115	9		1052
AVTSANIQEF	355	10		1053
AVGILLVVVL	657	11		1054
AWPDSLPLD	414	9	0.0041	1055
AYSLTLOGL	440	9	0.1300	1056
AYSLTLOGLI	440	11	0.0230	1057
AYVMAGYGSPY	771	11		1058
CFVHTVPW	475	8	0.0190	1059
CFVHTVPWDQL	475	11	0.0003	1060
CLFHNHSGI	255	9		1061
CLTSTVQL	789	8		1062
CMQIAKGM	826	8		1063
CMQIAKGMSY	826	10		1064
CMQIAKGMSYL	826	11	-0.0003	1065
CTGPKHSDCL	244	10		1066
CTGTDML	26	8		1067
CTGTDMLRL	26	10		1068
CTHSCVDL	630	8		1069
CTIDVYMI	947	8		1070
CTIDVYIM	947	9		1071
CVEECRVL	540	8		1072
CVEECRVLOGL	540	11		1073
CVGEGLACHQL	504	11		1074
CVNCSQFL	528	8		1075
CVTACPYN	295	9		1076
CVTACPYNYL	295	10		1077
CYGLGMEHL	342	9	0.0180	1078
CYQDTILW	162	8	0.0120	1079

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Table X
HER2/NEU A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
CYQDTLWKDI	162	11	0.0016	1080
DFGLARLL	863	8	0.0005	1081
DFGLARLLDI	863	10	0.0002	1082
DIFHKNNQL	171	9		1083
DIFHKNNQLAL	171	11		1084
DIQEVQGY	76	8		1085
DIQEVQGYVL	76	10		1086
DIQEVQGYVLI	76	11		1087
DLAARNVL	845	8		1088
DLGMGAAGKL	1089	10		1089
DLGPASPL	993	8		1090
DILLEKGERL	933	9		1091
DLNWCMI	821	9		1092
DLNWCMI	821	8		1093
DLNWCMI	821	11		1094
DLNWCMI	821	8		1095
DLNWCMI	821	10		1096
DLNWCMI	821	8		1097
DLNWCMI	821	9		1098
DLNWCMI	821	10		1099
DLNWCMI	821	11		1100
DLNWCMI	821	8		1101
DLNWCMI	821	9		1102
DLNWCMI	821	10		1103
DLNWCMI	821	11		1104
DLNWCMI	821	8		1105
DLNWCMI	821	10		1106
DLNWCMI	821	11		1107
DLNWCMI	821	8		1108
DLNWCMI	821	9		1109
DLNWCMI	821	10		1110
DLNWCMI	821	11		1111
DLNWCMI	821	8		1112
DLNWCMI	821	9		1113
DLNWCMI	821	10		1114
DLNWCMI	821	11		1115
DLNWCMI	821	8		1116
DLNWCMI	821	10		1117
DLNWCMI	821	11		1118
DLNWCMI	821	8		1119
DLNWCMI	821	10		1120
DLNWCMI	821	11		1121
DLNWCMI	821	8		1122
DLNWCMI	821	10		1123
DLNWCMI	821	11		1124
DLNWCMI	821	8		1125
DLNWCMI	821	10		1126
DLNWCMI	821	11		1127
DLNWCMI	821	8		1128
DLNWCMI	821	10		1129
DLNWCMI	821	11		1130
DLNWCMI	821	8		1131
DLNWCMI	821	10		1132
DLNWCMI	821	11		1133
DLNWCMI	821	8		1134
DLNWCMI	821	10		1135
DLNWCMI	821	11		1136
DLNWCMI	821	8		1137
DLNWCMI	821	10		1138
DLNWCMI	821	11		1139
DLNWCMI	821	8		1140
DLNWCMI	821	10		1141
DLNWCMI	821	11		1142
DLNWCMI	821	8		1143
DLNWCMI	821	10		1144
DLNWCMI	821	11		1145
DLNWCMI	821	8		1146
DLNWCMI	821	10		1147
DLNWCMI	821	11		1148
DLNWCMI	821	8		1149
DLNWCMI	821	10		1150
DLNWCMI	821	11		1151
DLNWCMI	821	8		1152
DLNWCMI	821	10		1153
DLNWCMI	821	11		1154
DLNWCMI	821	8		1155
DLNWCMI	821	10		1156
DLNWCMI	821	11		1157
DLNWCMI	821	8		1158
DLNWCMI	821	10		1159
DLNWCMI	821	11		1160
DLNWCMI	821	8		1161
DLNWCMI	821	10		1162
DLNWCMI	821	11		1163
DLNWCMI	821	8		1164
DLNWCMI	821	10		1165
DLNWCMI	821	11		1166
DLNWCMI	821	8		1167
DLNWCMI	821	10		1168
DLNWCMI	821	11		1169
DLNWCMI	821	8		1170
DLNWCMI	821	10		1171
DLNWCMI	821	11		1172
DLNWCMI	821	8		1173
DLNWCMI	821	10		1174
DLNWCMI	821	11		1175
DLNWCMI	821	8		1176
DLNWCMI	821	10		1177
DLNWCMI	821	11		1178
DLNWCMI	821	8		1179
DLNWCMI	821	10		1180
DLNWCMI	821	11		1181
DLNWCMI	821	8		1182
DLNWCMI	821	10		1183
DLNWCMI	821	11		1184
DLNWCMI	821	8		1185
DLNWCMI	821	10		1186
DLNWCMI	821	11		1187
DLNWCMI	821	8		1188
DLNWCMI	821	10		1189
DLNWCMI	821	11		1190
DLNWCMI	821	8		1191
DLNWCMI	821	10		1192
DLNWCMI	821	11		1193
DLNWCMI	821	8		1194
DLNWCMI	821	10		1195
DLNWCMI	821	11		1196
DLNWCMI	821	8		1197
DLNWCMI	821	10		1198
DLNWCMI	821	11		1199
DLNWCMI	821	8		1200
DLNWCMI	821	10		1201
DLNWCMI	821	11		1202
DLNWCMI	821	8		1203
DLNWCMI	821	10		1204
DLNWCMI	821	11		1205
DLNWCMI	821	8		1206
DLNWCMI	821	10		1207
DLNWCMI	821	11		1208
DLNWCMI	821	8		1209
DLNWCMI	821	10		1210
DLNWCMI	821	11		1211
DLNWCMI	821	8		1212
DLNWCMI	821	10		1213
DLNWCMI	821	11		1214
DLNWCMI	821	8		1215
DLNWCMI	821	10		1216
DLNWCMI	821	11		1217
DLNWCMI	821	8		1218
DLNWCMI	821	10		1219
DLNWCMI	821	11		1220
DLNWCMI	821	8		1221
DLNWCMI	821	10		1222
DLNWCMI	821	11		1223
DLNWCMI	821	8		1224
DLNWCMI	821	10		1225
DLNWCMI	821	11		1226
DLNWCMI	821	8		1227
DLNWCMI	821	10		1228
DLNWCMI	821	11		1229
DLNWCMI	821	8		1230
DLNWCMI	821	10		1231
DLNWCMI	821	11		1232
DLNWCMI	821	8		1233
DLNWCMI	821	10		1234
DLNWCMI	821	11		1235
DLNWCMI	821	8		1236
DLNWCMI	821	10		1237
DLNWCMI	821	11		1238
DLNWCMI	821	8		1239
DLNWCMI	821	10		1240
DLNWCMI	821	11		1241
DLNWCMI	821	8		1242
DLNWCMI	821	10		1243
DLNWCMI	821	11		1244
DLNWCMI	821	8		1245
DLNWCMI	821	10		1246
DLNWCMI	821	11		1247
DLNWCMI	821	8		1248
DLNWCMI	821	10		1249
DLNWCMI	821	11		1250
DLNWCMI	821	8		1251
DLNWCMI	821	10		1252
DLNWCMI	821	11		1253
DLNWCMI	821	8		1254
DLNWCMI	821	10		1255
DLNWCMI	821	11		1256
DLNWCMI	821	8		1257
DLNWCMI	821	10		1258
DLNWCMI	821	11		1259
DLNWCMI	821	8		1260
DLNWCMI	821	10		1261
DLNWCMI	821	11		1262
DLNWCMI	821	8		1263
DLNWCMI	821	10		1264
DLNWCMI	821	11		1265
DLNWCMI	821	8		1266
DLNWCMI	821	10		1267
DLNWCMI	821	11		1268
DLNWCMI	821	8		1269
DLNWCMI	821	10		1270
DLNWCMI	821	11		1271
DLNWCMI	821	8		1272
DLNWCMI	821	10		1273
DLNWCMI	821	11		1274
DLNWCMI	821	8		1275
DLNWCMI	821	10		1276
DLNWCMI	821	11		1277
DLNWCMI	821	8		1278
DLNWCMI	821	10		1279
DLNWCMI	821	11		1280
DLNWCMI	821	8		1281
DLNWCMI	821	10		1282
DLNWCMI	821	11		1283
DLNWCMI	821	8		1284
DLNWCMI	821	10		1285
DLNWCMI	821	11		1286
DLNWCMI	821	8		1287
DLNWCMI	821	10		1288
DLNWCMI	821	11		1289
DLNWCMI	821	8		1290
DLNWCMI	821	10		1291
DLNWCMI	821	11		1292
DLNWCMI	821	8		1293
DLNWCMI	821	10		1294
DLNWCMI	821	11		1295
DLNWCMI	821	8		1296
DLNWCMI	821	10		1297
DLNWCMI	821	11		1298
DLNWCMI	821	8		1299
DLNWCMI	821	10		1300
DLNWCMI	821	11		1301
DLNWCMI	821	8		1302
DLNWCMI	821	10		1303
DLNWCMI	821	11		1304
DLNWCMI	821	8		1305
DLNWCMI	821	10		1306
DLNWCMI	821	11		1307
DLNWCMI	821	8		1308
DLNWCMI	821	10		1309
DLNWCMI	821	11		1310
DLNWCMI	821	8		1311
DLNWCMI	821	10		1312
DLNWCMI	821	11		1313
DLNWCMI	821	8		1314
DLNWCMI	821	10		1315
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DLNWCMI	821	10		1318
DLNWCMI	821	11		1319
DLNWCMI	821	8		1320
DLNWCMI	821	10		1321
DLNWCMI	821	11		1322
DLNWCMI	821	8		1323
DLNWCMI	821	10		1324
DLNWCMI	821	11		1325
DLNWCMI	821	8		1326
DLNWCMI	821	10		1327
DLNWCMI	821	11		1328
DLNWCMI	821	8		1329
DLNWCMI	821	10		1330
DLNWCMI	821	11		1331
DLNWCMI	821	8		1332
DLNWCMI	821	10		1333
DLNWCMI	821	11		1334
DLNWCMI	821	8		1335
DLNWCMI	821	10		1336
DLNWCMI	821	11		1337
DLNWCMI	821	8		1338
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DLNWCMI	821	11		1340
DLNWCMI	821	8		1341
DLNWCMI	821	10		1342
DLNWCMI	821	11		1343
DLNWCMI	821	8		1344
DLNWCMI	821	10		1345
DLNWCMI	821	11		1346
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DLNWCMI	821	10		1348
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DLNWCMI	821	8		1350
DLNWCMI	821	10		1351
DLNWCMI	821	11		1352
DLNWCMI	821	8		1353
DLNWCMI	821	10		1354
DLNWCMI	821	11		1355
DLNWCMI	821	8		1356
DLNWCMI	821	10		1357
DLNWCMI	821	11		1358
DLNWCMI	821	8		1359
DLNWCMI	821	10		1360
DLNWCMI	821	11		1361
DLNWCMI	821	8		1362
DLNWCMI	821	10		1363
DLNWCMI	821	11		1364
DLNWCMI	821	8		1365
DLNWCMI	821	10		1366
DLNWCMI	821	11		1367
DLNWCMI	821	8		1368
DLNWCMI	821	10		1369
DLNWCMI	821	11		1370
DLNWCMI	821	8		1371

Table X
HER2/NEU A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
ETELVEPL	693	8		1129
ETHLDMRLHL	40	10		1130
ETHLDMRLHLY	40	11		1131
ETLEETGY	401	9		1132
ETLEETGYL	401	10		1133
ETLEETGYLY	401	11		1134
EVQGYVLI	79	8		1135
EYRAVTSANI	352	10		1136
EYHADGGKVP	876	11		1137
EYLVPOQGF	1022	9	-0.0003	1138
EYLVPOQGF	1022	10	0.0014	1139
EYVNAHCL	553	9	0.0120	1140
FLQDIQEVQGY	73	11	0.0061	1141
FTQSDVW	899	8		1142
FTQSDVWSY	899	10		1143
FVHTVPWDQL	476	10		1144
FVHTVPWDQLF	476	11		1145
FVYIQNEDL	986	9		1146
FYRSLEDDDD	1004	11		1147
GICELHCPAL	262	10		1148
GICLTSTVOL	787	10		1149
GILKRRQKI	672	11		1150
GILLVVVL	660	8		1151
GIPAREIPDL	925	10		1152
GIPAREIPDLL	925	11		1153
GISWGLRSL	449	10		1154
GLAIHHNTHL	464	11		1155
GLARLLDI	865	8		1156
GLGISWLGL	447	9		1157
GLRELQLRSL	136	10		1158
GLRSLREL	454	8		1159
GMGAAGKL	1091	8		1160
GMGAAGKLQSL	1091	11		1161
GMVLEDVRL	832	10		1162
GTDMLRL	28	8		1163
GTPAENPEY	1239	10		1164
GTPAENPEYL	1239	11		1165
GTQLFEDNY	104	9		1166
GTQLFEDNYAL	104	11		1167
GTYYKGIW	732	8		1168
GTYYKGIWI	732	9		1169
GVGSPYVSRL	776	10		1170
GVGSPYVSRL	776	11		1171
GVPDLSY	603	8		1172
GVPDLSYM	603	9		1173
GVPDLSYMPI	603	11		1174
GVLIQRNPQL	152	10		1175
GVTYWELM	909	8		1176
GVTYWELMTF	909	10		1177

Table X
HER2/NEU A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
GVVFGIL	668	8		1178
GVVKDVF	1179	9		1179
GYLYISAW	408	8	0.0044	1180
HFNHSGICEL	257	10	0.0002	1181
HLCFVHTVPW	473	10		1182
HLDMLRHL	42	8		1183
HLDMLRHLY	42	9		1184
HTVPWDQL	478	8		1185
HTVPWDQLF	478	9		1186
HVKITDFGL	858	9		1187
HVRENRGRL	809	9		1188
IFGSLAF	370	8	0.0120	1189
IFHKNNQL	172	8	-0.0003	1190
IFHKNNQLAL	172	10	0.0022	1191
IISAVVGI	654	8		1192
IISAVVGIL	654	9		1193
IISAVVGILL	654	10		1194
ILDEAYVM	767	8		1195
ILHNGAYSL	435	9		1196
ILHNGAYSLTL	435	11		1197
ILIKRRQKI	673	10		1198
ILKGGVLI	148	8		1199
ILLVVVLGVVF	661	11		1200
IMVKCMI	954	8	0.0210	1201
ITDFGLARL	861	9		1202
ITDFGLARLL	861	10		1203
ITGYLYISAW	406	10		1204
IVRGTLF	101	8		1205
IWPDGENVKI	738	11	0.0027	1206
KIFGSLAF	369	8		1207
KIFGSLAF	369	9		1208
KIPVAIKVL	747	9		1209
KIRKYMRRLL	681	10		1210
KIRKYMRRLL	681	11		1211
KITDFGLARL	860	10		1212
KITDFGLARLL	860	11		1213
KVKVLGSGAF	722	10		1214
KVLGSGAF	724	8		1215
KVPIKWMAL	883	9		1216
KWMALES	887	8	0.0080	1217
KWMALESIL	887	9	0.0150	1218
KYTMRRLL	684	8	0.0024	1219
LFEDNYAL	107	8	0.0006	1220
LFEDNYALAVL	107	11	0.0006	1221
LFRNPHQAL	485	9	0.0002	1222
LFRNPHQALL	485	10	0.0014	1223
LIHNTHL	467	8		1224
LIHNTHLCF	467	10		1225
LIKRRQKI	674	9		1226

Table X
HER2/NEU A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
LIQNPQL	154	8		1227
LIQNPQLCY	154	10		1228
LLDDETEY	869	9		1229
LLDDDDMGDL	1008	10		1230
LLEKGERL	934	8		1231
LLNWCMI	822	8		1232
LLQETELVEPL	690	11		1233
LLVVLGVVF	662	10		1234
LMPYGCLL	800	8	0.0076	1235
LMTGAKPY	915	9	0.0001	1236
LTCSPQPEY	1131	9		1237
LTEILKGGVL	145	10		1238
LTEILKGGVLI	145	11		1239
LTLQGLI	443	8		1240
LTLQGLISW	443	10		1241
LTLQGLISWL	443	11		1242
LTSISAVVGI	651	11		1243
LTSVQLVTQL	790	11		1244
LYLPTNASL	62	10		1245
LYDAEYL	1017	8		1246
LVEPLTPSGAM	696	11		1247
LVKSPNHVKI	852	10		1248
LVPOOGFF	1024	8		1249
LVSEFSRM	972	8		1250
LVTLQMPY	796	8		1251
LVTLQMPYGCL	796	11		1252
LVTYNTDTF	271	9		1253
LVVLGVVF	663	9		1254
LVVLGVVFGI	663	11		1255
LYISAWPDSL	410	10	0.0840	1256
MIDSECRPRF	960	10		1257
MIMVKCWM	953	8		1258
MIMVKCWM	953	9		1259
MIMVKCWM	953	8		1260
MTFGAKPY	916	8		1261
MTFGAKPYDGI	916	11		1262
NQEFAGCKKI	360	11		1263
NLOVIRGRI	427	9		1264
NLOVIRGRIL	427	10		1265
NTAPLQPEQL	388	10		1266
NTDTFESM	275	8		1267
NTSPKANKEI	758	10		1268
NTSPKANKEIL	758	11		1269
NVKIPVAL	745	8		1270
NVKIPVAIKVL	745	11		1271
NWCMQIAKGM	824	10	0.0002	1272
PICTIDVY	945	8		1273
PICTIDVYM	945	9		1274
PICTIDVYMI	945	10		1275
PICTIDVYMIM	945	11		

Table X
HER2/NEU A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
PIKWMALESI	885	10		1276
PIKWMALESIIL	885	11		1277
PINCTHSCVDL	627	11		1278
PLDSTFYRSL	999	10		1279
PLDSTFYRSL	999	11		1280
PLPSETDGY	1119	9		1281
PLQPEQLQVF	391	10		1282
PLTCSQPQPEY	1130	10		1283
PLTPSGAM	699	8		1284
PMCKGSRGW	197	9	0.0011	1285
PTAENPEY	1241	8		1286
PTAENPEYL	1241	9		1287
PTAENPEYLG	1241	11		1288
PTHDPSP	1102	8		1289
PTHDPSP	1102	11		1290
PTHDPSP	1102	11		1291
PTNASLSF	66	8		1292
PTNASLSFL	66	9		1293
PTQCVNCSQF	525	10		1294
PTQCVNCSQFL	525	11		1295
PVTGASPGGL	128	10		1296
PYDGIPAREI	922	10	0.0005	1297
PYVSRLGI	780	9	0.1700	1298
PYVSRLGICL	780	11	0.0320	1299
QIAKMSY	828	8		1300
QIAKMSYL	828	9		1301
QLCARGHCW	513	9		1302
QLCYQDTI	160	8		1303
QLCYQDTIL	160	9		1304
QLCYQDTILW	160	10		1305
QLFEDNYAL	106	9		1306
QLFRNPHOAL	484	10		1307
QLFRNPHQALL	484	11		1308
QLMPYGCL	799	8		1309
QLMPYGCLL	799	9		1310
QLQVFETL	396	8		1311
QLQVFETLEEI	396	11		1312
QLRSLTEI	141	8		1313
QLRSLTEIL	141	9		1314
QLVTQLMPY	795	9		1315
QMRILKETEL	711	10		1316
QVCTGDM	24	8		1317
QVCTGDMKL	24	10		1318
QVFETLEEI	398	9		1319
QVIRGRIL	429	8		1320
QVPLQRLRI	93	9		1321
QVRQVPLQRL	90	10		1322
QVQGNLEL	54	9		1323
QVQGNLELTY	54	11		1324
RFRELVSEF	968	9	0.0180	

Table X
HER2/NEU A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
RFTHQSDVW	898	9	0.0110	1325
RFTHQSDVWSY	898	11		1326
RFVYQIONEDL	985	10	0.0002	1327
RIHNGAY	434	8		1328
RIHNGAYSL	434	10		1329
RILKETEL	713	8		1330
RIVRGITQL	100	8		1331
RIVRGITQLF	100	9		1332
RLGSQDLL	816	8		1333
RLGSQDLLNW	816	10		1334
RLLDIDETV	868	10		1335
RLLDIDETV	689	8		1336
RLLOETEL	34	10		1337
RLPASPETHL	940	10		1338
RLPQPICTI	98	10		1339
RLRIVRGITQL	98	11		1340
RLRIVRGITQLF	98	9	0.0032	1341
RMARDPQRF	340	8		1342
RVCYGLGM	340	11		1343
RVCYGLGMEHL	340	10		1344
RVLOGLPREY	545	8	0.0250	1345
RWGLLLAL	8	9	1.3000	1346
RWGLLLALL	8	10	0.0120	1347
RYSEDPVPL	1111	10		1348
SIISAVVGI	653	9		1349
SIISAVVGIL	653	10		1350
SIISAVVGILL	653	11		1351
SLAFLPESF	373	9		1352
SLEDDDM	1007	8		1353
SLEDDDMGDL	1007	11		1354
SLPDLVSF	418	8		1355
SLPDLVSFQNL	418	11		1356
SLPTHDPSP	1100	10		1357
SLRELGSGL	457	9		1358
SLRELGSGLAL	457	11		1359
SLFLQDI	70	8		1360
SLTEILKGGVL	144	11		1361
SLTLQGLGI	442	9		1362
SLTLQGLGWS	442	11		1363
SMNPPEGRY	281	9	0.0001	1364
SMNPPEGRYTF	281	11	0.0180	1365
STDVGSCTL	305	9		1366
STFYRSLL	1002	8		1367
STQVCTGTD	22	10		1368
STRSGGDL	1051	9		1369
STRSGGDLTL	1051	11		1370
STVOLVTQL	792	9		1371
STVOLVTQLM	792	10		1372
SVFQNLQVI	423	9	-0.0003	1373
SWLGLRSL	451	8		

Table X
HER2/NEU A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
SWLGLRSLREL	451	11	0.0036	1374
SYGVTWVWEL	907	9	0.1200	1375
SYGVTWVWELM	907	10	0.0630	1376
SYLEDVRL	834	8	0.0059	1377
SYMPIWKF	609	8	0.3200	1378
TFGAKPYDGI	917	10	0.0002	1379
TIDVYMIM	948	8		1380
TILWKDIF	166	8		1381
TLEEITGY	402	8		1382
TLEEITGYL	402	9		1383
TLEEITGVLY	402	10		1384
TLEEITGYLYI	402	11		1385
TLERPKTL	1166	8		1386
TLOGLGISW	444	9		1387
TLOQLGISWL	444	10		1388
TMRRLLQETEL	686	11	-0.0003	1389
TVPLPSETDGY	1117	11		1390
TVPWDQLF	479	8		1391
TVQLVTQL	793	8		1392
TVQLVTQLM	793	9		1393
TVQLVTQLMPY	793	11		1394
TWELMTF	911	8		1395
TYKGIWI	733	8		1396
TYLPTNASL	63	9	0.0380	1397
TYLPTNASLSF	63	11	8.9000	1398
TYNTDTFESM	273	10	0.0074	1399
VFDGDLGM	1085	8	-0.0003	1400
VFETLEEI	399	8	-0.0003	1401
VFETLEEITGY	399	11	-0.0003	1402
VFQNLQVI	424	8		1403
VLDNGDPL	116	8		1404
VLGSAFGTVY	725	11		1405
VLGVVFGI	666	8		1406
VLGVVFGIL	666	9		1407
VLGVVFGILI	666	10		1408
VLIQNPOL	153	9		1409
VLIQNPQLCY	153	11		1410
VLOGLPREY	546	9		1411
VLKSPNHVKI	851	11		1412
VMAGVGSPY	773	9	0.0001	1413
VTACPNNY	296	8		1414
VTACPNNYL	296	9		1415
VTGASPGGL	129	9		1416
VTQLMPYGCL	797	10		1417
VTQLMPYGCLL	797	11		1418
VTSANIQEF	356	9		1419
VTWELMTF	910	9		1420
VTYNTDTF	272	8		1421
VTYNTDTFESM	272	11		1422

Table X
HER2/NEU A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
VVGILLVVVL	658	10		1423
VVIQNEDL	987	8		1424
VVKDVFAP	1180	8		1425
VVLGVVFGI	665	9		1426
VVLGWVFGIL	665	10		1427
VVLGVVFGILI	665	11		1428
VVQGNLEL	55	8		1429
VVQGNLELTY	55	10		1430
VVQGNLELTYL	55	11		1431
VVLGVVF	664	8		1432
VVLGVVFGI	664	10		1433
VVLGVVFGIL	664	11		1434
VWSYGVTVW	905	9		1435
VWSYGVTVWEL	905	11	0.0800	1436
VYIMVVKCW	951	9	0.0920	1437
VYIMVVKCWM	951	10	0.1600	1438
VYIMVVKCWMI	951	11	0.0220	1439
WIPDGENVKI	739	10	1.8000	1440
WLGLRSLREL	452	10		1441
WMALESIL	888	8	-0.0003	1442
WMIDSECRPRF	959	11	0.0011	1443
YISAWPDSL	411	9		1444
YLPINASL	64	8		1445
YLPINASLSF	64	10		1446
YLPINASLSFL	64	11		1447
YLPINASLSFL	64	11		1448
YLPINASLSFL	303	11		1449
YLPINASLSFL	1023	8		1450
YLPINASLSFL	1023	9		1451
YLPINASLSFL	409	11		1452
YLPINASLSFL	952	8	0.0009	1453
YLPINASLSFL	952	9		1454
YLPINASLSFL	952	10	0.0019	1455
YLPINASLSFL	772	10	0.0001	1456
YLPINASLSFL	554	8		1457
YLPINASLSFL	781	8		1458
YLPINASLSFL	781	10		

Table XI
HER2/NEU B07 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	B*0702	SEQ ID NO.
APGAGGMV	1036	8	1459	1459
APLQPEQL	390	8	1460	1460
APLQPEQLQV	390	10	1461	1461
APLQPEQLQVFF	390	11	1462	1462
APLTCSPQPEY	1129	11	1463	1463
APQHPHPPA	1204	9	1464	1464
APQHPHPPAF	1204	10	1465	1465
APSEGAGSDV	1076	10	1466	1466
APSEGAGSDVF	1076	11	1467	1467
CPAEQRASPL	642	10	1468	1468
CPDPAPGA	1032	8	1469	1469
CPDPAPGAGGM	1032	11	1470	1470
CPINCTHSCV	626	10	1471	1471
CPLHNQEV	315	8	1472	1472
CPLHNQEVTA	315	10	1473	1473
CPSGVKPDLL	600	9	1474	1474
CPSGVKPDLSY	600	11	1475	1475
CPYNLSTDV	299	10	1476	1476
DPAPGAGGM	1034	9	1477	1477
DPAPGAGGMV	1034	10	1478	1478
DPASNTAPL	384	9	1479	1479
DPLNNTTPV	121	9	1480	1480
DPQRFVVI	982	8	1481	1481
DPSPQLRY	1105	8	1482	1482
EPLTPSGA	698	8	1483	1483
EPLTPSGAM	698	9	1484	1484
GPASPLDSTF	995	10	1485	1485
GPASPLDSTFY	995	11	1486	1486
GPEADQCV	578	8	1487	1487
GPEADQCVVA	578	9	1488	1488
GPEADQCVACA	578	11	1489	1489
GPQPTQCV	522	8	1490	1490
GPKHSDCL	246	8	1491	1491
GPKHSDCLA	246	9	1492	1492
GPKHSDCLACL	246	11	1493	1493
GPLPAARPA	1155	9	1494	1494
GPLPAARPAGA	1155	11	1495	1495
GPTQCVNCSQF	524	11	1496	1496
HPECQPNQGSV	564	11	1497	1497
HPPAFSPA	1208	9	1498	1498
HPPAFSPAF	1208	10	1499	1499
IPAREIPDL	926	9	1500	1500
IPAREIPDLL	926	10	1501	1501
IPDGENVKI	740	9	1502	1502
IPDGENVKIPV	740	11	1503	1503
IPDLLEKGERL	931	11	1504	1504

Table XI
HER2/NEU B07 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	B*0702	SEQ ID NO.
IPVAKVL	748	8	1505	1505
KPCARVCY	336	8	1506	1506
KPCARVCYGL	336	10	1507	1507
KPDLSYMPI	605	9	1508	1508
KPDLSYMPIW	605	10	1509	1509
KPYDGIIPA	921	8	1510	1510
KPYDGIPAREI	921	11	1511	1511
LPAARPAGA	1157	9	1512	1512
LPAARPAGATL	1157	11	1513	1513
LPAETHL	35	9	1514	1514
LPAETHLDM	35	11	1515	1515
LPDLSVFQNL	419	10	1516	1516
LPESFDGPA	377	10	1517	1517
LPPGAASTQV	16	10	1518	1518
LPQPICTI	941	9	1519	1519
LPQPICTIDV	941	11	1520	1520
LPREYVNA	550	8	1521	1521
LPSETDGY	1120	8	1522	1522
LPSETDGYV	1120	9	1523	1523
LPSETDGYVA	1120	10	1524	1524
LPDCCHEQCA	231	11	1525	1525
LPTHDPSP	1101	9	1526	1526
LPTNASLSF	65	9	1527	1527
LPTNASLSFL	65	10	1528	1528
MPNPEGRY	282	8	1529	1529
MPNPEGRYTF	282	10	1530	1530
MPNQAQMIRI	706	9	1531	1531
MPNQAQMIRIL	706	10	1532	1532
MPYGCLLDHV	801	10	1533	1533
NPEGRYTF	284	8	1534	1534
NPEGRYTFGA	284	10	1535	1535
NPEYLGLDV	1245	9	1536	1536
NPEYLGLDVPV	1245	11	1537	1537
NPEYLTQGGG	1193	11	1538	1538
NPHQALLHTA	488	10	1539	1539
NPQLCYQDTI	158	10	1540	1540
NPQLCYQDTIL	158	11	1541	1541
PFAFSPAF	1210	8	1542	1542
PFAFSPAFDNL	1210	11	1543	1543
PPERGAAPPSTF	1227	11	1544	1544
PPGAASTQV	17	9	1545	1545
PICTIDV	944	8	1546	1546
PICTIDVY	944	9	1547	1547
PICTIDVYM	944	10	1548	1548
PICTIDVYMI	944	11	1549	1549
PPAFSPA	1209	8	1550	1550

Table XI
HER2/NEU B07 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	B*0702	SEQ ID NO.
PPPAFSPAF	1209	9	1551	1551
PPSPREGPL	1149	9	1552	1552
PPSPREGPLPA	1149	11	1553	1553
PPSTFKGTPTA	1233	11	1554	1554
QPEQLQVF	393	8	1555	1555
QPEQLQVFETL	393	11	1556	1556
QPEYVNQPDV	1136	10	1557	1557
QHPPPAF	1206	8	1558	1558
QHPPPAFSPA	1206	11	1559	1559
QPPICTIDV	943	9	1560	1560
QPPICTIDVY	943	10	1561	1561
QPPICTIDVYM	943	11	1562	1562
QPSPREGPL	1148	10	1563	1563
QPONGSVTCF	568	10	1564	1564
RPEDECVGEG	499	11	1565	1565
RPRFREL	966	8	1566	1566
RPRFREL	966	11	1567	1567
RPRFREL	966	11	1568	1568
SPAFDNL	1214	8	1569	1569
SPAFDNL	1214	9	1570	1570
SPAFDNL	1214	10	1571	1571
SPETHLDM	38	8	1572	1572
SPETHLDM	38	9	1573	1573
SPGGLREL	133	8	1574	1574
SPGGLREL	133	10	1575	1575
SPGKNGV	1174	8	1576	1576
SPGKNGV	1174	11	1577	1577
SPGKNGV	1174	11	1578	1578
SPKANK	760	8	1579	1579
SPKANK	760	9	1580	1580
SPLAPSEGA	1073	9	1581	1581
SPLDSTFY	998	8	1582	1582
SPLDSTFY	998	11	1583	1583
SPLTSISA	649	9	1584	1584
SPLTSISAV	649	10	1585	1585
SPLTSISAV	649	11	1586	1586
SPMCKGRCW	196	10	1587	1587
SPNHVKITDF	855	10	1588	1588
SPREGPLA	1151	9	1589	1589
SPREGPLA	1151	10	1590	1590
SPVSRLL	779	8	1591	1591
SPVSRLL	779	10	1592	1592
TPSGAMPNQA	701	10	1593	1593
TPTAENPEY	1240	9	1594	1594
TPTAENPEYL	1240	10	1595	1595
TPVTGASPGGL	127	11	1596	1596
VPIKWMAL	884	8		
VPIKWMAL	884	11		

Table XI
HER2/NEU B07 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	B*0702	SEQ ID NO.
VPLPSETDGY	1118	10	1597	1597
VPLPSETDGYV	1118	11	1598	1598
VPLQRLRI	94	8	1599	1599
VPLQRLRIV	94	9	1600	1600
WPDSLPLDL	415	8	1601	1601
WPDSLPLDLNV	415	10	1602	1602
WPDSLPLDLNVF	415	11	1603	1603

Table XII
HER2/NEU B27 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AHNOVRQVPL	87	10	1604
AHYKDPFF	588	8	1605
ARCPGVKPD	598	11	1606
ARDPQRFVVI	980	10	1607
AREIPDLL	928	8	1608
ARLLDIDET	867	11	1609
ARPAGATL	1160	8	1610
ARVCYGLM	339	9	1611
CHQLCARGHCW	511	11	1612
CKKIFGSL	367	8	1613
CKKIFGSLAF	367	10	1614
CKKIFGSLAF	367	11	1615
CRPRFREL	965	8	1616
CRVLQGLPREY	544	11	1617
CRWGLLLAL	7	9	1618
CRWGLLLAL	7	10	1619
DHVRENRGR	808	10	1620
EKGERLPQPI	936	11	1621
ERGAPPSTF	1229	9	1622
ERLPQPI	939	8	1623
ERLPQPICTI	939	11	1624
FKNNQLAL	173	9	1625
FKNNQLALTL	173	11	1626
FRELVSF	969	8	1627
FRELVSFMR	969	11	1628
FRNPQAL	486	8	1629
FRNPQAL	486	9	1630
GKNGVVDVF	1176	10	1631
GKVPKWM	882	8	1632
GKVPKWMAL	882	10	1633
GRILHNGAY	433	9	1634
GRILHNGAYSL	433	11	1635
GRLSQDL	815	8	1636
GRLSQDL	815	9	1637
GRLSQDLN	815	11	1638
HNTHLCF	469	8	1639
HNTHLCF	174	8	1640
HNTHLCF	174	10	1641
HNTHLCF	174	11	1642
HRDLAARNVL	843	10	1643
HNTHLCF	468	9	1644
IKRQKI	675	8	1645
IKRQKIRKY	675	11	1646
IKWMALES	886	9	1647
IKWMALES	886	10	1648
IKRILHNGAY	431	11	1649

Table XII
HER2/NEU B27 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
IRKYTEMRRL	682	9	1650
IRKYTMRRLL	682	10	1651
KHSDCLACL	248	9	1652
KHSDCLACLFH	248	11	1653
KKIFGSLAF	368	9	1654
KKIFGSLAF	368	10	1655
KRQOKIRKY	676	10	1656
LHCPALVTY	266	9	1657
LHFNHSGI	256	8	1658
LHFNHSGICEL	256	11	1659
LHNGAYSL	436	8	1660
LHNGAYSLTL	436	10	1661
LRELGSGL	458	8	1662
LRELGSGLAL	458	10	1663
LRELGSGLALI	458	11	1664
LRELQLRSL	137	9	1665
LRIVRGTQL	99	9	1666
LRIVRGTQLF	99	10	1667
LRLPASPETHL	33	11	1668
LRLRELGSGL	455	11	1669
LRLTEIL	142	8	1670
MRILKETEL	712	9	1671
MRLLQETEL	687	10	1672
NHSGICEL	259	8	1673
NHVKITDF	857	8	1674
NHVKITDFGL	857	10	1675
NKEILDEAY	764	9	1676
NKEILDEAYVM	764	11	1677
NRGRLGSDLL	813	10	1678
NRGRLGSDLL	813	11	1679
PHPPAFSPAF	1207	11	1680
PKANKEIL	761	8	1681
PKHSDCLACL	247	10	1682
PREYNARHCL	551	11	1683
PRFREL VSEF	967	10	1684
QKIRKYTM	680	8	1685
QKIRKYTMRRLL	680	11	1686
QRASPLTSI	646	9	1687
QRASPLTSII	646	10	1688
QRFVVIQNEDL	984	11	1689
QRLRIVRGTL	97	11	1690
QRNPQLCY	156	8	1691
QRYSEDPTVPL	1110	11	1692
RKVKVLGSGAF	721	11	1693
RKYTMRRLL	683	8	1694
RKYTMRRLL	683	9	1695

Table XII
HER2/NEU B27 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
RRFTHQSDVW	897	10	1696
RRLQETEL	688	9	1697
RRQKIRKY	677	9	1698
RRQKIRKYTM	677	11	1699
RRFTHQSDVW	896	11	1700
SKPCARVCY	335	9	1701
SKPCARVCYGL	335	11	1702
SRACHPCSPM	189	10	1703
SRLLGICL	783	8	1704
SRMARDPQRF	977	10	1705
THDPSPLQRY	1103	10	1706
THLCFVHTVPW	472	11	1707
THLDMRLHL	41	9	1708
THLDMRLHLY	41	10	1709
THOSDVWSY	900	10	1710
TRSGGGDL	1052	8	1711
TRSGGGDLTL	1052	10	1712
VHRDLAARNVL	842	11	1713
VHTVPWDQL	477	9	1714
VHTVPWDQLF	477	10	1715
VKIPVAIKVL	746	10	1716
VKITDFGL	859	8	1717
VKITDFGLARL	859	11	1718
VKPDLSYM	604	8	1719
VKPDLSYMPI	604	10	1720
VKPDLSYMPIW	604	11	1721
VKSPNHVKI	853	9	1722
VKVLGSGAF	723	9	1723
VRAVTSANI	353	9	1724
VRENRGRL	810	8	1725
VRGTQLFEDNY	102	11	1726
VRLVHRDL	839	8	1727
VRQVPLQRL	91	9	1728
VRQVPLQRLRI	91	11	1729
WKDIFHKNNQL	169	11	1730
YHADGGKVPI	877	10	1731
YRSLEDDDM	1005	10	1732

Table XIII
HER2/NEU B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AAKGLQSL	1094	8	1733
AALCRWGL	4	8	1734
AALCRWGGL	4	9	1735
AALCRWGLLL	4	10	1736
AAPQPPPPAF	1203	11	1737
AARPAGATL	1159	9	1738
ASCVTACPY	293	9	1739
ASCVTACPYNY	293	11	1740
ASLFLQDI	69	9	1741
ASPETHLDM	37	9	1742
ASPETHLDM	37	10	1743
ASPGGLREL	132	9	1744
ASPGGLREL	132	11	1745
ASPGGLRELQL	997	8	1746
ASPLDSTF	997	9	1747
ASPLDSTFY	997	8	1748
ASPLTSII	648	11	1749
ASPLTSISAV	648	11	1750
ASTOVCTGTD	21	9	1751
ATLERPKTL	1165	9	1752
CAHYKDPPE	587	11	1753
CAHYKDPPECV	587	8	1754
CARCKGPL	224	8	1755
CARVGYGL	338	10	1756
CARVGYGLM	338	8	1757
CSKPCARV	334	10	1758
CSKPCARVCY	334	11	1759
CSPMCKGSRW	195	8	1760
CSPQPEYV	1133	11	1761
CSQFLRQECV	531	10	1762
CTGPKHSDCL	244	8	1763
CTGTDML	26	10	1764
CTGTDMLRL	26	8	1765
CTHSCVDL	630	8	1766
CTIDVYMI	947	9	1767
CTIDVYMI	947	10	1768
CTIDVYMI	947	11	1769
CTIDVYMI	947	8	1770
DSECRPRF	962	11	1771
DSECRPRFREL	962	8	1772
DSLPLDSV	417	9	1773
DSLPLDSVF	417	8	1774
DSTFYRSL	1001	9	1775
DSTFYRSL	1001	8	1776
DTILWKDI	165	9	1777
DTILWKDIF	165	11	1778
EADQCVACAHY	580	8	
EAYVMAGV	770		

Table XIII
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Sequence	Position	No. of Amino Acids	SEQ ID NO.
ESILRRRF	892	8	1779
ESMPNPEGRY	280	10	1780
ESSEDCQSL	207	9	1781
ETDGYVAPL	1123	9	1782
ETELRKVKV	717	9	1783
ETELRKVKVL	717	10	1784
ETELVEPL	693	8	1785
ETEHADGGKV	874	11	1786
ETHLDMLRHL	40	10	1787
ETHLDMLRHLY	40	11	1788
ETLEEITGY	401	9	1789
ETLEEITGYL	401	10	1790
ETLEEITGYLY	401	11	1791
FAGCKKIF	364	8	1792
FAGCKKIIFGSL	364	11	1793
FSPAFDNL	1213	8	1794
FSPAFDNL	1213	9	1795
FSPAFDNL	1213	10	1796
FSPAFDNL	1213	11	1797
FSPAFDNL	1213	11	1798
FSRMARDPQRF	976	8	1799
FTHQSDVW	899	10	1800
FTHQSDVWSY	899	9	1801
GAAGKQSL	1093	8	1802
GACQPCPI	621	10	1803
GAFTGYKGI	729	11	1804
GAFTGYKGIW	729	11	1805
GAGSDVFDGDL	1080	8	1806
GAKPYDGI	919	9	1807
GAMPNQAQM	704	11	1808
GAMPNQAQMRI	704	10	1809
GASCVTACPY	292	10	1810
GASPGGLREL	131	10	1811
GATLERPKTL	1164	8	1812
GAVENPEY	1189	9	1813
GAYSLTLQGL	439	10	1814
GSCTLVCPPL	309	9	1815
GSDVFDGDL	1082	11	1816
GSDVFDGDLGM	1082	8	1817
GSGAFGTV	727	9	1818
GSGAFGTVY	727	10	1819
GSLAFLPESF	372	8	1820
GSPYVSRLL	778	9	1821
GSPYVSRLLGI	778	11	1822
GSQDLINW	818	8	1823

Table XIII
HER2/NEU B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
GSODLLNWCM	818	10	1825
GTDMLRL	28	8	1826
GTPTAENPEY	1239	10	1827
GTPTAENPEYL	1239	11	1828
GTQLFEDNY	104	9	1829
GTQLFEDNYAL	104	11	1830
GTVYKGIW	732	8	1831
GTVYKGIWI	732	9	1832
HADGKGVPI	878	9	1833
HADGKGVPIKW	878	11	1834
HSDCLACL	249	8	1835
HSDCLACLHF	249	10	1836
HTANRPEDECY	495	11	1837
HTVPWDQL	478	8	1838
HTVPWDQLF	478	9	1839
IAHNOVRQV	86	9	1840
IAHNOVRQVPL	86	11	1841
IAKGMSYL	829	8	1842
IAKGMSYLEDV	829	11	1843
ISAVYGIL	655	8	1844
ISAVYGILL	655	9	1845
ISAVYGILLV	655	10	1846
ISAVYGILLVV	655	11	1847
ISAWPDSL	412	8	1848
ISAWPDSL	412	11	1849
ISAWPDSLPL	450	9	1850
ISWGLRSL	450	9	1851
ITDFGLARL	861	10	1852
ITDFGLARLL	861	10	1853
ITGYLYISAW	406	11	1854
KANKEILDEAY	762	11	1855
KSPNHVKI	854	8	1856
KSPNHVKITDF	854	11	1857
KTLSPGKNGV	1171	10	1858
KTLSPGKNGVV	1171	11	1859
LAALCRWGL	3	9	1860
LAALCRWGILL	3	10	1861
LAALCRWGILLL	3	11	1862
LAARNLV	846	8	1863
LACLFHNSGI	253	11	1864
LAFLPESF	374	8	1865
LALIHNTHL	465	10	1866
LAPSEGAGSDV	1075	11	1867
LAVLDNGDPL	114	10	1868
LFLQDIQEV	71	10	1869
LSPGKNGV	1173	8	1870
LSPGKNGVV	1173	9	

Table XIII
HER2/NEU B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
LSTDVGSCTL	304	10	1871
LSTDVGSCTLV	304	11	1872
LSVFQNLQV	422	9	1873
LSVFQNLQVI	422	10	1874
LSYMPIWKF	608	9	1875
LTCSPQPEY	1131	9	1876
LTCSPQPEYV	1131	10	1877
LTEILKGGV	145	9	1878
LTEILKGGVL	145	10	1879
LTEILKGGVLI	145	11	1880
LTLQGLGI	443	8	1881
LTLQGLGISW	443	10	1882
LTLQGLGISWL	443	11	1883
LTSISAV	651	8	1884
LTSISAVV	651	9	1885
LTSISAVVGI	651	11	1886
LTSIVQLV	790	8	1887
LTSIVQLVTQL	790	11	1888
LYLPTNASL	62	10	1889
MAGVGSPP	774	8	1890
MAGVGSPPV	774	9	1891
MALESILRRRF	889	11	1892
MARDPQRF	979	8	1893
MARDPQRFV	979	9	1894
MARDPQRFVV	979	10	1895
MARDPQRFVVI	979	11	1896
MSYLEDVRL	833	9	1897
MSYLEDVRLV	833	10	1898
MTFGAKPY	916	8	1899
MTFGAKPYDGI	916	11	1900
NASLSFLQDI	68	10	1901
NTAPLQPEQL	388	10	1902
NTDTFESM	275	8	1903
NTHLCFVHTV	471	10	1904
NTSPKANKEI	758	10	1905
NTSPKANKEIL	758	11	1906
PAARPAGATL	1158	10	1907
PAEQRASPL	643	9	1908
PAFDNLYY	1215	8	1909
PAFDNLYYW	1215	9	1910
PAFSPAFDNL	1211	10	1911
PAFSPAFDNLV	1211	11	1912
PALVTYNTDTF	269	11	1913
PAPGAGGM	1035	8	1914
PAPGAGGMV	1035	9	1915
PAREPDL	927	8	1916

Table XIII
HER2/NEU B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
PAREIPDLL	927	9	1917
PASNTAPL	385	8	1918
PASPETHL	36	8	1919
PASPETHLDM	36	10	1920
PASPETHLDMML	36	11	1921
PASPLDSTF	996	9	1922
PASPLDSTFY	996	10	1923
PSEEEAPRSPL	1065	11	1924
PSEGAGSDV	1077	9	1925
PSEGAGSDVF	1077	10	1926
PSETDGYV	1121	8	1927
PSETDGYVAPL	1121	11	1928
PSGAMPNQAQM	702	11	1929
PSGVKPD	601	8	1930
PSGVKPDLSY	601	10	1931
PSGVKPDLSYM	601	11	1932
PSREGPL	1150	8	1933
PTAENPEY	1241	8	1934
PTAENPEYL	1241	9	1935
PTAENPEYGL	1241	11	1936
PTHDPSP	1102	8	1937
PTHDPSPQLQRY	1102	11	1938
PTNASLSF	66	8	1939
PTNASLSFL	66	9	1940
PTQCVNCSQF	525	10	1941
PTQCVNCSQFL	525	11	1942
QSDVWSYGV	902	9	1943
QSDVWSYGVTV	902	11	1944
QSLPTHDPSP	1099	11	1945
RACHPCSPM	190	9	1946
RASPLTSI	647	8	1947
RASPLTSII	647	9	1948
RAVTSANI	354	8	1949
RAVTSANIQEF	354	11	1950
RSGGDLTL	1053	9	1951
RSGGDLTLGL	1053	11	1952
RSLEDDDM	1006	9	1953
RSLELGSGL	456	10	1954
RSLELKGCV	143	11	1955
RSRACHPCSPM	188	11	1956
SAVVGILL	656	8	1957
SAVVGILLV	656	9	1958
SAVVGILLVV	656	10	1959
SAVVGILLVVV	656	11	1960
SAWPDLSL	413	10	1961
SAWPDLSLPDL	413	10	1962
SSEDCQSL	208	8	

Table XIII
HER2/NEU B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
SSSTRSGGDL	1049	11	1963
SSSTRSGGDL	1050	10	1964
STDVGSCTL	305	9	1965
STDVGSCTLV	305	10	1966
STFYRSLL	1002	8	1967
STQVCTGDM	22	10	1968
STRSGGDL	1051	9	1969
STRSGGDLTL	1051	11	1970
STVQLVTQL	792	9	1971
STVQLVTQLM	792	10	1972
TACPYNL	297	8	1973
TAENPEYL	1242	8	1974
TAENPEYLG	1242	10	1975
TANRPEDEV	496	10	1976
TAPLQPEQL	389	9	1977
TAPLQPEQLQV	389	11	1978
TSANIQEF	357	8	1979
TSIISAVV	652	8	1980
TSIISAVVGI	652	10	1981
TSIISAVVGIL	652	11	1982
TSPKANKEI	759	9	1983
TSPKANKEIL	759	10	1984
TSTVQLVTQL	791	10	1985
TSTVQLVTQLM	791	11	1986
VACAHYKDPF	585	11	1987
VARCPGV	597	8	1988
VSRLGICL	782	9	1989
VTACPYN	296	8	1990
VTACPYNL	296	9	1991
VTGASFGGL	129	9	1992
VTQLMPYGCL	797	10	1993
VTQLMPYGCLL	797	11	1994
VTSANIQEF	356	9	1995
VTVWELMTF	910	9	1996
VTYNTDTF	272	8	1997
VTYNTDTFESM	272	11	1998
WSYGVTVW	906	8	1999
WSYGVTVWEL	906	10	2000
WSYGVTVWELM	906	11	2001
YSEDPTVPL	1112	9	2002
YSLTLQGL	441	8	2003
YSLTLQGLGI	441	10	2004
YTFGASCV	289	8	2005

Table XIV
HER2/NEU B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
ALESILRRRF	890	10	2006
ALIHNTLHLCF	466	11	2007
ALVTYNTDTF	270	10	2008
AMPNQAQM	705	8	2009
AMPNQAQMRI	705	10	2010
APGAGGMV	1036	8	2011
APLQPEQLQV	390	10	2012
APLQPEQLQVF	390	11	2013
APLTCSRQPEY	1129	11	2014
APQHPPPAF	1204	10	2015
APSEGAGSDV	1076	10	2016
APSEGAGSDVF	1076	11	2017
AVTSANIQEF	355	10	2018
AVVGILLV	657	8	2019
AVVGILLV	657	9	2020
AVVGILLVVV	657	10	2021
CLHFNHSGI	255	9	2022
CLTSTVQLV	789	9	2023
CMQIAKGM	826	8	2024
CMQIAKGMSY	826	10	2025
CPDPAPGAGGM	1032	11	2026
CPINCTHSCV	626	10	2027
CPLHNQEV	315	8	2028
CPSGVKPDLSY	600	11	2029
CPYNLSTDV	299	10	2030
CQPQNGSV	567	8	2031
CQPQNGSVTCF	567	11	2032
CQSLTRTV	212	8	2033
CVARCPGV	596	9	2034
CVTACPYNV	295	9	2035
DIQEVQGY	76	8	2036
DIQEVQGYV	76	9	2037
DIQEVQGYVLI	76	11	2038
DLAARNVLV	845	9	2039
DLNWCMI	821	9	2040
DLSVFQNLQV	421	10	2041
DLSVFQNLQVI	421	11	2042
DLSYMPTW	607	8	2043
DLSYMPTWK	607	10	2044
DLVDAEY	1016	8	2045
DLVDAEYLV	1016	10	2046
DMGDLVDAEY	1013	11	2047
DPAPGAGGM	1034	9	2048
DPAPGAGGMV	1034	10	2049
DPLNNTTPV	121	9	2050
DPQRFVVI	982	8	2051

Table XIV
HER2/NEU B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
DSPLORY	1105	8	2052
DQCACAHY	582	9	2053
DVFAFGAV	1183	9	2054
DVFDGDLGM	1084	9	2055
DVGSCTLV	307	8	2056
DWVSYGTV	904	9	2057
DWVSYGTVW	904	10	2058
DVMIMVKCW	950	10	2059
DVMIMVKCWM	950	11	2060
ELDEAYV	766	8	2061
ELDEAYVM	766	9	2062
ELKGGVLI	147	9	2063
EITGYLYT	405	8	2064
EITGYLYTSAW	405	11	2065
ELAALCRW	2	8	2066
ELGGLALI	460	9	2067
ELHCPALV	265	8	2068
ELHCPALVTY	265	10	2069
ELMTFGAKPY	914	10	2070
ELQLRSLTEI	139	10	2071
ELYSEFSRM	971	9	2072
EPLTPSGAM	698	9	2073
EQRASPLTSI	645	10	2074
EQRASPLTSII	645	11	2075
EVQGYVLI	79	8	2076
EVRAVTSANI	352	10	2077
FLDQIEV	73	8	2078
FLDQIEVQGY	73	11	2079
FLRGOECV	534	8	2080
FQNLQVIRGRI	425	11	2081
FVHTVPWDOLF	476	11	2082
GICELHCPALV	262	11	2083
GICLTSTV	787	8	2084
GICLTSTVQLV	787	11	2085
GILIKRRQKI	672	11	2086
GILLVVVLGV	660	10	2087
GILLVVVLGVV	660	11	2088
GIWPDGENV	737	10	2089
GLARLLDI	865	8	2090
GLGMEHLREV	344	10	2091
GMEHLREV	346	8	2092
GMEHLREVRAV	346	11	2093
GMSYLEDV	832	8	2094
GMSYLEDVRLV	832	11	2095
GPASPLDSTF	995	10	2096
GPASPLDSTFY	995	11	2097

Table XIV
HER2/NEU B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
GPEADQCV	578	8	2098
GPQTQCV	522	8	2099
GPTQVNCQSF	524	11	2100
GQECVEECRV	537	10	2101
GKPDLSY	603	8	2102
GKPDLSYM	603	9	2103
GKPDLSYMPI	603	11	2104
GVTWELM	909	8	2105
GVTWELMTF	909	10	2106
GVVFGIL	668	8	2107
GVVKDVF	1179	9	2108
HLCFVHTV	473	8	2109
HLCFVHTVPW	473	10	2110
HLDMLRLHY	42	9	2111
HLREVRV	349	8	2112
HLVQGCQV	48	8	2113
HLVQGCQV	48	9	2114
HPQCQNGSV	564	11	2115
HPPAFSPAF	1208	10	2116
HQLCARGHCW	512	10	2117
HQSDVWSY	901	8	2118
HQSDVWSYGV	901	10	2119
IISAVVGI	654	8	2120
IISAVVGILLV	654	11	2121
ILDEAYVM	767	8	2122
ILDEAYVMAGV	767	11	2123
ILKRRQKI	673	10	2124
ILKETELRKV	714	10	2125
ILKGGVLI	148	8	2126
ILLVVVLGV	661	9	2127
ILLVVVLGV	661	10	2128
ILLVVVLGVVF	661	11	2129
IMVKCWM	954	8	2130
IPDGENVKI	740	9	2131
IPDGENVKIPV	740	11	2132
IQEFACGCKI	361	10	2133
IQEFACGCKIIF	361	11	2134
IOEVQGVY	77	8	2135
IOEVQGVYLI	77	10	2136
IQRNPOLCY	155	9	2137
IVRGTQLF	101	8	2138
KIFGSLAF	369	8	2139
KIPVAIKV	747	8	2140
KPCARVCY	336	8	2141
KPDLSYMPI	605	9	2142
KPDLSYMPIW	605	10	2143

Table XIV
HER2/NEU B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
KPYDGIPIREI	921	11	2144
KVKVLGSGAF	722	10	2145
KVLGSGAF	724	8	2146
KVLGSGAFGTV	724	11	2147
LIAHNOVROV	85	10	2148
LIHNTHLCF	467	10	2149
LIHNTHLCFV	467	11	2150
LIKRRQOKI	674	9	2151
LIQRNPQLCY	134	10	2152
LLDIDETEV	869	9	2153
LLDDDDMGDLV	1008	11	2154
LLGICLTSTV	785	10	2155
LLNWCMQI	822	8	2156
LLPPGAASTQV	15	11	2157
LLQETELV	690	8	2158
LLVVVLGV	662	8	2159
LEVVLGVV	662	9	2160
LLVVVLGVWF	662	10	2161
LMPYGCLLDHV	800	11	2162
LMTFGAKPY	915	9	2163
LPASPETHLDM	35	11	2164
LPFGAASTQV	16	10	2165
LPQPICTI	941	9	2166
LPQPICTIDV	941	11	2167
LPSETDGY	1120	8	2168
LPSETDGYV	1120	9	2169
LPTNASLSF	65	9	2170
LDIQEVQGY	74	10	2171
LDIQEVQGYV	74	11	2172
LQGLGWS	445	8	2173
LQGLPREY	547	8	2174
LQGLPREYV	547	9	2175
LQLSLTEI	140	9	2176
LQEQQLQV	392	8	2177
LQEQQLQVF	392	9	2178
LQRYSEDPTV	1109	10	2179
LQVFETLEEI	397	10	2180
LOVIRGRI	428	8	2181
LVCPLHNOEV	313	10	2182
LVDAAEYLV	1017	9	2183
LVEPLTPSGAM	696	11	2184
LVHRDLAARNV	841	11	2185
LVKSPNHV	852	8	2186
LVKSPNHVKI	852	10	2187
LVPOQGF	1024	8	2188
LVSEFSRM	972	8	2189

Table XIV
HER2/NEU B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
LVTLMPY	796	8	2190
LVTYNTDTF	271	9	2191
LVVVLGVV	663	8	2192
LVVVLGVVF	663	9	2193
LVVVLGVVFGI	663	11	2194
MIDSECRPRF	960	10	2195
MIMVKCWM	953	8	2196
MIMVKCWM	953	9	2197
MLRHLVQGCQV	45	11	2198
MPNPEGRY	282	8	2199
MPNPEGRYTF	282	10	2200
MPNQAQMRI	706	9	2201
MPYGCLLDHV	801	10	2202
MQIAKMSY	827	9	2203
NIQEFAGCKKI	360	11	2204
NLQVIRGRI	427	9	2205
NPECRYTF	284	8	2206
NPEYLGLDV	1245	9	2207
NPEYLGLDVPV	1245	11	2208
NPQLCYQDTI	158	10	2209
NQLALTLI	177	8	2210
NKIPVAI	745	8	2211
NVKIPVAIKV	745	10	2212
NVLVKSPNHV	850	10	2213
PICTIDVY	945	8	2214
PICTIDVYM	945	9	2215
PICTIDVYMI	945	10	2216
PICTIDVYMIM	945	11	2217
PIKWMALESI	885	10	2218
PINCTHSCV	627	9	2219
PLNNTTPV	122	8	2220
PLPSETDGY	1119	9	2221
PLPSETDGYV	1119	10	2222
PLQPEQLQV	391	9	2223
PLQPEQLQVF	391	10	2224
PLQRLRIV	95	8	2225
PLQRYSEDPTV	1108	11	2226
PLTCSPOPEY	1130	10	2227
PLTCSPOPEYV	1130	11	2228
PLTSPGAM	699	8	2229
PLTSISAV	650	9	2230
PLTSISAVV	650	10	2231
PMCKGSRGW	197	9	2232
PPAFSPAF	1210	8	2233
PPERGAPPSTF	1227	11	2234
PPGAASTQV	17	9	2235

Table XIV
HER2/NEU B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
PICTIDV	944	8	2236
PICTIDVY	944	9	2237
PICTIDVYM	944	10	2238
PICTIDVYMI	944	11	2239
PPAFSPAF	1209	9	2240
POLCYQDTI	159	9	2241
PQLCYQDTILW	159	11	2242
PONGSVTCF	569	9	2243
PQPEYVNPQDV	1135	11	2244
PQPHPPAF	1205	9	2245
PQPPICTI	942	8	2246
PQPPICTIDV	942	10	2247
PQPPICTIDVY	942	11	2248
QIAKMSY	828	8	2249
QLCARGHCW	513	9	2250
QLCYQDTI	160	8	2251
QLCYQDTILW	160	10	2252
QLFEDNYALAV	106	11	2253
QLQVFETLEI	396	11	2254
QLRSLTEI	141	8	2255
QLVTQLMPY	795	9	2256
QPEQLQVF	393	8	2257
QPEYVNPQDV	1136	10	2258
QPHPPAF	1206	8	2259
QPICTIDV	943	9	2260
QPICTIDVY	943	10	2261
QPICTIDVYM	943	11	2262
QPNGSVTCF	568	10	2263
QOKIRKYTEM	679	9	2264
QVCTGDTM	24	8	2265
QVFETLEI	398	9	2266
QVPLQRLI	93	9	2267
QVPLQRLRIV	93	10	2268
QVVOGNLELTY	54	11	2269
RILHNGAY	434	8	2270
RILKETELRKV	713	11	2271
RIVRGTLF	100	9	2272
RLGSODLLNW	816	10	2273
RLLDIDETEV	868	10	2274
RLGLCLTSTV	784	11	2275
RLLOETELV	689	9	2276
RLPQPPICTI	940	10	2277
RLRIVRGTLF	98	11	2278
RMARDPQRF	978	9	2279
RMARDPQRFV	978	10	2280
RMARDPQRFVV	978	11	2281

Table XIV
HER2/NEU B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
RPRFREL	966	8	2282
RPRFRELSEF	966	11	2283
RQKIRKY	678	8	2284
RQKIRKYTM	678	10	2285
RQVPLQLRLI	92	10	2286
RQVPLQLRLIV	92	11	2287
RVCYGLGM	340	8	2288
RVLOGLPREY	545	10	2289
RVLOGLPREYV	545	11	2290
SIISAVVGI	653	9	2291
SLAFLPESF	373	9	2292
SLEDDDM	1007	8	2293
SLPDLSVF	418	8	2294
SLSFLQDI	70	8	2295
SLSFLQDIQEV	70	11	2296
SLTEILKGGV	144	10	2297
SLTLQGLGI	442	9	2298
SLTLQGLGISW	442	11	2299
SMNPEGRY	281	9	2300
SMNPEGRYTF	281	11	2301
SPAFDNL	1214	8	2302
SPAFDNL	1214	9	2303
SPAFDNL	1214	10	2304
SPAFDNL	1214	10	2305
SPETHLDM	38	8	2306
SPGKNGV	1174	8	2307
SPGKNGVVDV	1174	11	2308
SPKANKEI	760	8	2309
SPLDSTFY	998	8	2310
SPLTSISAV	649	10	2311
SPLTSISAVV	649	11	2312
SPMCKGSRGW	196	10	2313
SPNHVKITDF	855	10	2314
SPYVSRLLGI	779	10	2315
SQDLLNWCMI	819	9	2316
SQDLLNWCMI	819	11	2317
SQFLRGQECV	532	10	2318
SVFQNLQV	423	8	2319
SVFQNLQV	423	9	2320
TIDVYMM	948	8	2321
TIDVYMMV	948	9	2322
TILWKDIF	166	8	2323
TLEETGY	402	8	2324
TLEETGYLY	402	10	2325
TLEETGYLYI	402	11	2326
TLQGLGISW	444	9	2327
TLSPGKNGV	1172	9	

Table XIV
HER2/NEU B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
TLSPGKNGVV	1172	10	2328
TLVCPLHNOEV	312	11	2329
TPTAENPEY	1240	9	2330
TOCVNCSQF	526	9	2331
TQLFEDNY	105	8	2332
TOVCTGTDN	23	9	2333
TVPLPSETDGY	1117	11	2334
TVPWQDLF	479	8	2335
TVQLVTQLM	793	9	2336
TVQLVTQLMPY	793	11	2337
TVWELMTF	911	8	2338
TVYKGIWI	733	8	2339
VLGSGAFGTV	725	10	2340
VLGSGAFGTVY	725	11	2341
VLGVVFGI	666	8	2342
VLGVVFGILI	666	10	2343
VLIAHNOV	84	8	2344
VLIAHNQVRQV	84	11	2345
VLIQRNPQLCY	153	11	2346
VLOGLPREY	546	9	2347
VLOGLPREYV	546	10	2348
VLVKSPNHV	851	9	2349
VLVKSPNHVKI	851	11	2350
VMAGVGSPY	773	9	2351
VMAGVGSPYV	773	10	2352
VPIKWMALESI	884	11	2353
VPLPSETDGY	1118	10	2354
VPLPSETDGYV	1118	11	2355
VPLQLRLI	94	8	2356
VPLQLRLIV	94	9	2357
VQGNLELY	56	8	2358
VQLVTQLM	794	9	2359
VQLVTQLMPY	794	10	2360
WGILLV	658	8	2361
WGILLVVV	658	9	2362
VVKDVFAP	1180	8	2363
VVLGVVFGI	665	9	2364
VVLGVVFGILI	665	11	2365
WQGNLELY	55	10	2366
VVLGVVF	664	8	2367
VVLGVVFGI	664	10	2368
WIPDGENV	739	8	2369
WIPDGENYKI	739	10	2370
WMIDSECRPRF	959	11	2371
WPDSLPLDSV	415	10	2372
WPDSLPLDSVF	415	11	2373

Table XIV
HER2/NEU B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
YLEDVRLV	835	8	2374
YLGLDVPV	1248	8	2375
YLPTNASLSF	64	10	2376
YLPQQGF	1023	8	2377
YLPQQGFF	1023	9	2378
YMIMVKCW	952	8	2379
YMIMVKCWM	952	9	2380
YMIMVKCWMI	952	10	2381
YQDTILWKDI	163	10	2382
YQDTILWKDIF	163	11	2383
YVLAHNOV	83	9	2384
YVMAGVGSPY	772	10	2385
YVMAGVGSPYV	772	11	2386
YVSRLLGI	781	8	2387

Table XV
HER2/NEU A01 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0.101	SEQ ID NO.
AFSPAFDNLY	1212	10	0.0010	2388
AFSPAFDNLY	1212	11	0.0140	2389
ASCVTACPY	293	9	0.0550	2390
ASCVTACPYNY	293	11	0.1900	2391
ASPLDSTFY	997	9	0.0290	2392
CMQIAKMSY	826	10	0.3000	2393
CPSGVKPDLSY	600	11		2394
CSKPCARVCY	334	10	0.0016	2395
DMGDLVDAEY	1013	11	0.0027	2396
DPSPLQRY	1105	8		2397
EADQCVACAHY	580	11	0.1000	2398
ESMPNPEGRY	280	10	0.1800	2399
ETHLDMRLRHL	40	11	0.2800	2400
ETLEETGY	401	9	0.0430	2401
ETLEETGYLY	401	11	0.4400	2402
FESMPNPEGRY	279	11	0.0049	2403
FGASCVTACPY	291	11	0.0100	2404
FSPAFDNLY	1213	9	0.0430	2405
FSPAFDNLY	1213	10	5.5000	2406
FTHQSDVWSY	899	10	2.7000	2407
GASCVTACPY	292	10	0.0012	2408
GGAVENPEY	1188	9		2409
GPASPLDSTFY	995	11		2410
GSGAFGTVY	727	9	0.0011	2411
GTPTAENPEY	1239	10	0.0630	2412
GTQLFEDNY	104	9	0.1800	2413
HLDMLRHL	42	9	9.1000	2414
HQSDVWSY	901	8	-0.0021	2415
KCSKPCARVCY	333	11	-0.0017	2416
LEEITGYLY	403	9	0.0057	2417
LSGAFGTVY	726	10	0.0010	2418
LLDIDETGY	869	9	7.6000	2419
LMTFGAKPY	915	9	0.0011	2420
LPSETDGY	1120	8		2421
LODIOEVQGY	74	10	0.0015	2422
LTCSPQPEY	1131	9	0.1300	2423
MGDLVDAEY	1014	10	0.0120	2424
MTFGAKPY	916	8	-0.0021	2425
NKEILDEAY	764	9	0.0017	2426
PASPLDSTFY	996	10	0.0150	2427
PSGVKPDLSY	601	10	0.0010	2428
PTAENPEY	1241	8	0.0030	2429
PTHDPSPLOQRY	1102	11	0.0160	2430
QIAKMSY	828	8	-0.0021	2431
SGAFGTVY	728	8	-0.0021	2432
SMPNPEGRY	281	9	0.0028	2433
SPAFDNLY	1214	8		2434

Table XV
HER2/NEU A01 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
SPAFDNLYY	1214	9		2435
TCSPQPEY	1132	8	-0.0021	2436
THDPSPLQRY	1103	10	0.0015	2437
TLEEITGY	402	8	-0.0021	2438
TLEEITGYLY	402	10	1.1000	2439
VFETLEEITGY	399	11	0.0045	2440
VMAGVGSPY	773	9	0.0400	2441
VTACPYNV	296	8	0.1000	2442

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
AAGCTGPK	241	8		2443
AAGCTGPKH	241	9		2444
AAKGLQLPTH	1094	11		2445
AAICRWGLLLA	4	11		2446
AAQPHPPPA	1203	10		2447
AAQPHPPPAF	1203	11		2448
AARNVLVK	847	8		2449
AARPAATLER	1159	11		2450
ACAHYKDPFF	586	10		2451
ACHPCSPMCK	191	10		2452
ACHQLCAR	510	8		2453
ACHQLCARGH	510	10		2454
ACQPCPNCNH	622	11		2455
ADGKVPK	879	9		2456
ADQVACA	581	8		2457
ADQCVACAH	581	9		2458
ADQCVACAHY	581	10		2459
ADQCVACAHYK	581	11		2460
AFGGAVENPEY	1186	11		2461
AFSPAFDNLV	1212	10	0.0003	2462
AFSPAFDNLVY	1212	11		2463
AGATLERPK	1163	9		2464
AGCKKIFGSLA	365	11		2465
AGCTGPKH	242	8		2466
AGGCARCK	221	8		2467
AGGMVHHR	1039	8		2468
AGGMVHHRH	1039	9		2469
AGGMVHHRHR	1039	10		2470
AGVGSPPYSR	775	10		2471
ALCRWGLLLA	5	10		2472
ALESILRR	890	8		2473
ALESILRRR	890	9	0.0013	2474
ALESILRRRF	890	10		2475
ALIHNT	466	8		2476
ALIHNTHLCF	466	11		2477
ALLHTANR	492	8		2478
ALLPPGAA	14	8		2479
ALTLDITNR	180	9	0.0004	2480
ALTLDITNRSR	180	11		2481
ALVTYNTDTF	270	10		2482
AMPNQAQMR	705	9	0.0004	2483
ASCVTACPY	293	9	0.0008	2484
ASCVTACPNY	293	11		2485
ASPETHDMLR	37	11		2486
ASPLDSTF	997	8		2487
ASPLDSTFY	997	9	0.0002	2488

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
ASPLDSTFYR	997	10	0.0003	2489
ASPLTSIISA	648	10		2490
AVTSANIQEF	355	10		2491
AVTSANIQEF	355	11		2492
CAAGCTGPK	240	9	0.0021	2493
CAAGCTGPKH	240	10		2494
CAGGCARCK	220	9	-0.0002	2495
CAHYKDPFF	587	9		2496
CCHEQCAA	235	8		2497
CFGPEADQCV	576	11		2498
CLACLHFNH	252	9		2499
CLLDHVREN	805	10	0.0003	2500
CMQIAKMSY	826	10	0.0003	2501
CSKPCARVCY	334	10	0.0003	2502
CSPMCKGSR	195	9	-0.0008	2503
CTGPKHSDCLA	244	11		2504
CTGDMKLR	26	9	0.0002	2505
CTHSCVDLDDK	630	11		2506
CTIDVYMIMVK	947	11		2507
CTLVCPPLH	311	8		2508
CVACAHYK	584	8		2509
CVARCPGK	596	10	0.0220	2510
CVDLDDKGC	634	11		2511
CVGEGLAH	504	9		2512
CVNCSQFLR	528	9	0.0015	2513
CVTACPYNY	295	9	0.0002	2514
DCCHEQCA	234	8		2515
DCCHEQCAA	234	9		2516
DCLACLHF	251	8		2517
DCLACLHFNH	251	10		2518
DCQSLTRTVCA	211	11		2519
DDMGDLVDA	1011	10		2520
DDKGCPEQR	638	10		2521
DDKGCPEQRA	638	11		2522
DDMGDLVDA	1012	9		2523
DGDLGMA	1087	8		2524
DGDLGMAA	1087	9		2525
DGDLGMAAK	1087	10		2526
DGDPASNTA	382	9		2527
DGENWKIPVA	742	10		2528
DGGKVPK	880	8		2529
DGGKVPKWMA	880	11		2530
DGTQRCEK	326	8		2531
DGTQRCEKCSK	326	11		2532
DIDETEYH	871	8		2533
DIDETEYHA	871	9		2534

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
DIFHKNQLA	171	10		2535
DIOEVQGY	76	8		2536
DLAARNVLVK	845	10	0.0018	2537
DLDDKGCPA	636	9		2538
DLGMAAK	1089	8		2539
DILLEKGER	933	8		2540
DLNWCMIQIA	821	10		2541
DLNNWCMQIAK	821	11		2542
DLSYMPIWK	607	9	0.0005	2543
DLSTMPWK	607	10		2544
DLVDAAEY	1016	8		2545
DMGDLVDA	1013	8		2546
DMGDLVDAEY	1013	11		2547
DMKLRLPA	30	8		2548
DSECRPRF	962	8		2549
DSECRPRFR	962	9	-0.0002	2550
DSLPLDSVF	417	9		2551
DTILWKDIF	165	9		2552
DTILWKDIFH	165	10		2553
DTILWKDIFHK	165	11		2554
DTNRSRACH	185	9		2555
DVFAFGGA	1183	8		2556
DVFDGDLGMGA	1084	11		2557
DVRLVHRDLA	838	10		2558
DVRLVHRDLAA	838	11		2559
DVRPQPSPR	1144	10	0.0003	2560
DVYMIMVK	950	8		2561
EADQCVACA	580	9		2562
EADQCVACAH	580	10		2563
EADQCVACAHY	580	11		2564
EAPRSPLA	1069	8		2565
ECRVLQGLPR	543	10		2566
ECVGEGLA	503	8		2567
ECVGEGLACH	503	10		2568
EDCQSLTR	210	8		2569
EDDDMGDLVDA	1010	11		2570
EDECVGEGLA	501	10		2571
EDGTORCEK	325	9		2572
EDVRLVHR	837	8		2573
EDVRLVHRDLA	837	11		2574
EFAGCKKIF	363	9		2575
EFMRMARDPQR	975	11		2576
EGAGSDVF	1079	8		2577
EGLACHQLCA	507	10		2578
EGLACHQLCAR	507	11		2579
EGPLPAAR	1154	8		2580

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
EGPLPAARPA	1154	10		2581
EGRYTFCA	286	8		2582
EILDEAYVMA	766	10		2583
EILKGGVLIQR	147	11		2584
EIPDLLEK	930	8		2585
EIPDLLEKGER	930	11		2586
EITGYLYISA	405	10		2587
ELGSGIALIH	460	10		2588
ELGSGIALIIH	460	11		2589
ELHCPALVTY	265	10	0.0002	2590
ELMTFGAK	914	8		2591
ELMTFGAKPY	914	10	0.0002	2592
ELTYLPTNA	61	9		2593
ELVEPLTPSOA	695	11		2594
ELVSEFSR	971	8		2595
ELVSEFSRMA	971	10		2596
ELVSEFSRMAR	971	11		2597
ELVSEFSRMA	379	8		2598
ESFDGDPA	892	8		2599
ESILRRRF	892	10		2600
ESILRRRFTH	892	9	0.0003	2601
ESMPNPEGR	280	10	0.0003	2602
ESMPNPEGRY	280	11		2603
ESSEDCQSLTR	207	11		2604
ETELRKVK	717	8	0.0003	2605
ETEHYADGK	874	10		2606
ETHLDMLR	40	8		2607
ETHLDMLRH	40	9		2608
ETHLDMLRHL	40	11		2609
ETLEBITGY	401	9	0.0002	2610
ETLEBITGYLY	401	11		2611
EVQGYVLIH	79	9		2612
EVRAVTS	352	8		2613
EVTAEEDGTQR	321	10		2614
FAGCKKIF	364	8	0.0002	2615
FCPDAPGA	1031	9		2616
FCVARCPGSK	595	11		2617
FDGDLGMGA	1086	9		2618
FDGDLGMGA	1086	10		2619
FDGDLGMGA	1086	11		2620
FDGDLGMGA	1086	10		2621
FDGDLGMGA	1086	11		2622
FDGDLGMGA	1030	10		2623
FDGDLGMGA	1030	11		2624
FGAKPYDGIPA	918	8		2625
FGASCVT	291	11		2626
FGASCVTACPY	291	10		2627
FGA VENPEY	1187	10		2628

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
FGLIKRR	671	8		2627
FGLIKRRQK	671	11		2628
FGPEADQCVA	577	10		2629
FGSLAFLPESF	371	11		2630
FLPESFDGDP	376	11		2631
FLDQIEVOGY	73	11		2632
FSPAFDNL	1213	9	0.0002	2633
FSPAFDNL	1213	10	0.0005	2634
FSRMDPQRF	976	10	-0.0002	2635
FSRMDPQRF	976	11		2636
FTQSDVWSY	899	10	0.0003	2637
FVHTVPDQLF	476	11		2638
GAAPQHPHPPA	1202	11		2639
GAFGTVYK	729	8		2640
GAGGMVHH	1038	8		2641
GAGGMVHHR	1038	9	-0.0002	2642
GAGGMVHHRH	1038	10		2643
GAGGMVHHRH	1038	11		2644
GAKPYDGIPA	919	10		2645
GAKPYDGIPAR	919	11		2646
GAMPNQAQMR	704	10	-0.0002	2647
GAPSTFK	1231	8		2648
GASCVTACPY	292	10	0.0003	2649
GASPGGLR	131	8		2650
GATLERPK	1164	8		2651
GAVENPEY	1189	8		2652
GCKKIFGSLA	366	10		2653
GCKKIFGSLAF	366	11		2654
GCLLDHVR	804	8		2655
GCLLDHVREN	804	11		2656
GCPAEQRA	641	8		2657
GDLGMGAA	1088	8		2658
GDLGMGAAG	1088	9		2659
GDLVDAEY	1015	9		2660
GDPASNTA	383	8		2661
GFPCPDPA	1029	8		2662
GFPCPDPA	1029	11		2663
GGAPQPH	1201	8	0.0003	2664
GGAVENPEY	1188	9		2665
GKVPKWMMA	881	10		2666
GGLRELQLR	135	9		2667
GGMVHHRH	1040	8		2668
GGMVHHRH	1040	9		2669
GICELHCPA	262	9		2670
GILIKRRQK	672	10	0.0150	2671
GISWLGLR	449	8		2672

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
GISWGLRSLR	449	11		2673
GIWPDGENVK	737	11		2674
GLACHQLCA	508	9		2675
GLACHQLCAR	508	10	0.0110	2676
GLALIHNTH	464	10		2677
GLEPSEEA	1062	9		2678
GLEPSEEAAPR	1062	11		2679
GLGISWGLR	447	10	0.0037	2680
GLGMEHLR	344	8		2681
GLGMEHLREVR	344	11		2682
GLLLALLPPGA	10	11		2683
GLPREYVNA	549	9		2684
GLPREYVNAR	549	10	0.0002	2685
GLPREYVNARH	549	11		2686
GLQSLPTH	1097	8		2687
GLRELQLR	136	8		2688
GMEHLREVR	346	9	-0.0002	2689
GMEHLREVRA	346	10		2690
GMSYLEDVR	832	9	-0.0002	2691
GMVHRHR	1041	8		2692
GSCTLVCPLH	309	10		2693
GSGAFGTYY	727	9	0.0028	2694
GSGAFGTYYK	727	10	0.0660	2695
GSLALIH	462	8		2696
GSLALIIH	462	9		2697
GSLAFLPESF	372	10		2698
GSVTCFGPEA	572	10		2699
GTDMLRLRPA	28	10		2700
GTPTAENPEY	1239	10	0.0002	2701
GTQLFEDNY	104	9	0.0001	2702
GTQLFEDNYA	104	10		2703
GTORCEKCSK	327	10	0.0210	2704
GVGSPYVSR	776	9	0.0010	2705
GVKPDLSY	603	8		2706
GTVVWELMTF	909	10		2707
GVVFGILIK	668	9	0.0047	2708
GVVFGILIKR	668	10	0.0180	2709
GVVFGILIKRR	668	11		2710
GVVKDVFA	1179	8		2711
GVVKDVFAF	1179	9		2712
HADGKVKPIK	878	10	0.0003	2713
HCPALVTY	267	8		2714
HDPSPLOQR	1104	8		2715
HDPSPLOQR	1104	9		2716
HFNHSIGICELH	257	11		2717
HLDMLRHL	42	9	0.0370	2718

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
HLREVRVYTS	349	11		2719
HSCVLDLDDK	632	9	-0.0002	2720
HSDCLACLIH	249	9		2721
HSDCLACLFH	249	10		2722
HSGICELH	260	8		2723
HSGICELHCPA	260	11		2724
HTVPWDQLF	478	9		2725
HTVPWDQLFR	478	10	0.0035	2726
HVKITDFGLA	858	10		2727
HVKITDFGLAR	858	11		2728
HVRENRRGR	809	8		2729
ICELHCPA	263	8		2730
IDETEHYA	872	8		2731
IDSECRPR	961	8		2732
IDSECRPRF	961	9		2733
IDSECRPRFR	961	10		2734
IDTNRSA	184	8		2735
IDTNRSRACH	184	10		2736
IDVYMIMVK	949	9		2737
IFHKNNQLA	172	9		2738
ILDEAYYMA	767	9	0.3800	2739
ILIKRROOK	673	9		2740
ILIKRRQOKIR	673	11		2741
ILKETELR	714	8	0.0190	2742
ILKETELRK	714	9		2743
ILKETELRKVK	714	11		2744
ILKGGVLQIR	148	10	0.0400	2745
ILLVVVLGVVF	661	11		2746
ILRRRFTH	894	8		2747
ILWKDIFH	167	8		2748
ILWKDIFHK	167	9	0.2800	2749
ISWLGRLSLR	450	10	0.0410	2750
ITDFGLAR	861	8		2751
ITGYLYISA	406	9		2752
IVRGTLF	101	8		2753
KANKEILDEA	762	10		2754
KANKEILDEAY	762	11		2755
KCSKPCAR	333	8		2756
KCSKPCARVCY	333	11		2757
KCWMDSECR	957	10		2758
KDIFHKNNQLA	170	11		2759
KDPPFCVA	591	8		2760
KDPPFCVAR	591	9		2761
KDVFAFGGA	1182	9		2762
KPDEEGA	615	8		2763
KCPAEQR	640	8		2764

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
KGCPAEQRA	640	9		2765
KGVLQIR	150	8		2766
KGQSLPTH	1096	9		2767
KGMSYLEQVR	831	10		2768
KGPLPTDCCH	228	10		2769
KGPTAENPEY	1238	11		2770
KIFGSLAF	369	8		2771
KIPVAIKVLR	747	10	0.0009	2772
KIRKVTMR	681	8	0.0010	2773
KIRKVTMR	681	9	0.7600	2774
KITDEGLA	860	8		2775
KITDFGLR	860	9	0.1700	2776
KLRLPASPETH	32	11		2777
KSPNHVKITDF	854	11		2778
KVKVLGSGA	722	9		2779
KVKVLGSGAF	722	10		2780
KVLGSGAF	724	8		2781
KVLENTSPK	753	10	0.3800	2782
KVLENTSPK	753	11		2783
KVLENTSPKA	753	11		2784
KVPIKWMA	883	8		2785
LAARNVLVK	846	9	0.0580	2786
LACHQLCA	509	8	-0.0002	2787
LACHQLCAR	509	9		2788
LACHQLCARGH	509	11		2789
LACLHFNH	253	8		2790
LAFLPESF	374	8		2791
LALIHNTNTH	465	9		2792
LALLPGCA	13	8		2793
LALLPGAA	13	9		2794
LALTIDTNR	179	10		2795
LCRWGLLA	6	9	-0.0002	2796
LCYODTILWK	161	10		2797
LDDKGCPC	637	8		2798
LDDKGCPCAEQR	637	11		2799
LDEAYVMA	768	8	0.0081	2800
LDHVRENK	807	8		2801
LDHVRENRR	807	10		2802
LDIDETEH	870	8		2803
LDIDETEH	870	9		2804
LDIDETEH	870	10		2805
LDMLRHLY	43	8		2806
LFEDNYALA	107	9		2807
LFRNPHQA	485	8		2808
LFRNPHQALLH	485	11		2809
LGISWLGLR	448	9		2810
LGLEPSEEEA	1061	10		

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	Δ^*0301	SEQ ID NO.
LGMEHLREVR	345	10		2811
LGMEHLREVRA	345	11		2812
LGPASPLDSTF	994	11		2813
LGSGAFGTVY	726	10	0.0003	2814
LGSGAFGTVYK	726	11		2815
LGSGLALIH	461	9		2816
LGSGLALIIH	461	10		2817
LGWVFGILIK	667	10		2818
LGWVFGILIKR	667	11		2819
LIAHQVR	85	8		2820
LIDTNRSR	183	8		2821
LIDTNRRA	183	9		2822
LIDTNRSRACH	183	11		2823
LHHNTHLCF	467	10		2824
LIKRRQOK	674	8	0.0002	2825
LIKRRQOKIR	674	10		2826
LIKRRQOKIRK	674	11		2827
LIQNPOLCY	674	10	0.0012	2828
LLALLPPGA	154	10		2829
LLALLPPGA	12	9		2830
LLALLPPGAA	12	10	0.0370	2831
LLDHVRENH	806	9		2832
LLDHVRENHGR	806	11	0.0003	2833
LLDIDETEV	869	9		2834
LLDIDETEVH	869	10		2835
LLDIDETEVHA	869	11		2836
LLALLPPGA	11	10		2837
LLALLPPGAA	11	11		2838
LLNWCMIQA	822	9	0.1400	2839
LLNWCMIQAK	822	10		2840
LLVVLGVVF	662	10		2841
LMFYGCLLDH	800	10		2842
LMTFGAKPY	915	9	0.0002	2843
LSPGKNGVVK	1173	10	-0.0002	2844
LSVFQNLQVIR	422	11		2845
LSYMPIWK	608	8		2846
LSYMPIWK	608	9	0.0001	2847
LTCSPQPEY	1131	9		2848
LTIDTNR	181	8	0.0002	2849
LTIDTNRSR	181	10		2850
LTIDTNRRA	181	11		2851
LTPQGGAA	1197	8		2852
LTPSGAMPNQA	700	11		2853
LTRTVACAGCA	215	11		2854
LTYLPTNA	62	8		2855
LVEPLTPSGA	696	10		2856
LVRDLAA	841	8		

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
LVHRDLAAR	841	9	0.0040	2857
LVKSPNHVK	852	9	0.4800	2858
LVPOQGF	1024	8		2859
LVSEFSRMA	972	9		2860
LVSEFSRMAR	972	10	0.0072	2861
LVTLQMPY	796	8		2862
LVTYNTDTF	271	9		2863
LVVVLGVVF	663	9		2864
MAGVGSPY	774	8		2865
MAGVGSPYVSR	774	11		2866
MALESILR	889	8		2867
MALESILRR	889	9	0.0034	2868
MALESILRRR	889	10	0.0011	2869
MALESILRRRF	889	11		2870
MARDPQRF	979	8		2871
MGDLVDAEEY	1014	10	0.0002	2872
MIDSECRPR	960	9	0.0017	2873
MIDSECRPRF	960	10		2874
MIDSECRPRFR	960	11		2875
MSYLEDVR	833	8		2876
MSYLEDVRLVH	833	11		2877
MTFGAKPY	916	8		2878
NARHCLPCH	556	9		2879
NGSVTCFGPEA	571	11		2880
NGVVKDVF	1178	8		2881
NGVVKDVFA	1178	9		2882
NGVVKDVFAF	1178	10		2883
NIQEFAGCK	360	9	0.0002	2884
NIQEFAGCKK	360	10	0.0003	2885
NLELTLYPTNA	59	11		2886
NLQVIRGR	427	8		2887
NLQVIRGRILH	427	11		2888
NTHLCFVH	471	8		2889
NTSPKANK	758	8		2890
NTTPVTGA	125	8		2891
NVKIPVAIK	745	9	0.0038	2892
NVLKSPNH	850	9		2893
NVLKSPNHVK	850	11		2894
PAARPAGA	1158	8		2895
PAFDNLYY	1215	8		2896
PAFSPAFDNLY	1211	11		2897
PAGATLER	1162	8		2898
PAGATLERPK	1162	10	-0.0002	2899
PALVTYNTDTF	269	11		2900
PAPGAGGMVH	1035	10		2901
PAPGAGGMVHH	1035	11		2902

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
PAREIPDLEK	927	11		2903
PASPLDSTF	996	9		2904
PASPLDSTFY	996	10	0.0003	2905
PASPLDSTFYR	996	11		2906
PCPNCCTH	625	8		2907
PCSPMCKGSR	194	10		2908
PDGENVKIPVA	741	11		2909
PDLEKGER	932	9		2910
PDSLVMPIWK	606	10		2911
PDSLVMPIWKF	606	11		2912
PDSLPLDSVF	416	10		2913
PDYRQPSPR	1143	11		2914
PGAGGMVH	1037	8		2915
PGAGGMVHH	1037	9		2916
PGAGGMVHHR	1037	10		2917
PGAGGMVHHRH	1037	11		2918
PGGLRELQLR	134	10		2919
PGKNGVVK	1175	8		2920
PGKNGVVKDVF	1175	11		2921
PICTIDVY	945	8		2922
PIWKFDEGA	612	11		2923
PLAPSEGA	1074	8		2924
PLDSTFYR	999	8		2925
PLHNQEVTA	316	9		2926
PLNNTTPVTGA	122	11		2927
PLPAARPA	1156	8		2928
PLPAARPAGA	1156	10	0.0002	2929
PLPSETDGY	1119	9		2930
PLPSETDGYVA	1119	11		2931
PLPTDCCH	230	8		2932
PLQPEQLQVF	391	10		2933
PLQRLRIVR	95	9	0.0002	2934
PLTCSQPQPEY	1130	10	0.0002	2935
PLTSHISA	650	8		2936
PSEEEAPR	1065	8		2937
PSEGAGSDVF	1077	10		2938
PSETDGYVA	1121	9		2939
PSGAMPNQA	702	9	0.0003	2940
PSGVKPDLSY	601	10		2941
PSREGPLPA	1150	10		2942
PSREGPLPAA	1150	11		2943
PSTFKGTPTA	1234	10		2944
PTAENPEY	1241	8		2945
PTDCCHEOCA	232	10		2946
PTDCCHEQCAA	232	11		2947
PTHDPSPLQR	1102	10	0.0003	2948

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
PTHDPSLQRY	1102	11		2949
PTNASLSF	66	8		2950
PTQVNCNQF	525	10		2951
PVAIKVLR	749	8		2952
PVTGASPGGLR	128	11		2953
QALLHTANR	491	9		2954
QAQMRILK	709	8	0.0046	2955
QCAAGCTGPK	239	10		2956
QCAAGCTGPKH	239	11		2957
QCVACAHY	583	8		2958
QCVACAHYK	583	9		2959
QVNCNQF	527	8		2960
QVNCNQFLR	527	10		2961
QDIQEVQY	75	9		2962
QDLLNWCMIQIA	820	11		2963
QDPPERGA	1225	8		2964
QDTILWKDIF	164	10		2965
QDTILWKDIFH	164	11		2966
QGFECFDPDA	1028	9		2967
QGGAAPOPH	1200	9		2968
QGLQISWGLR	446	11		2969
QGLPREYVNA	548	10		2970
QGLPREYVNAR	548	11		2971
QGNLELY	57	8		2972
QGVVLIH	81	8		2973
QIAKMSY	828	8		2974
QLALTIDTNR	178	11		2975
QLCYQDTILWK	160	11		2976
QLFEDNYA	106	8		2977
QLFEDNYALA	106	10		2978
QLFRNPHQA	484	9		2979
QLMPYGCILLDH	799	11		2980
QLSLTEILK	141	10	0.2000	2981
QLVTQLMPY	795	9	0.0110	2982
QMRILKETELR	711	11		2983
QSLTRTYCA	213	9		2984
QVCTGDMK	24	9	0.0007	2985
QVCTGDMKLR	24	11		2986
QVIRGRILH	429	9		2987
QVPLQLR	93	8		2988
QVPLQLRLRIVR	93	11		2989
QVRQVPLQR	90	9	0.0029	2990
QVRQVPLQRLR	90	11		2991
QVQGNLELY	54	11		2992
RACHPCSPMCK	190	11		2993
RASPLTSIISA	647	11		2994

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
RAVTSANIQEF	354	11		2995
RCEKCSKPCA	330	10		2996
RCEKCSKPCAR	330	11		2997
RDLAARNVLVK	844	11		2998
RFRELVSEF	968	9		2999
RFRELVSEFSR	968	11		3000
RFTHQSDVWSY	898	11		3001
RGAPPSTF	1230	8		3002
RGAPPSTFK	1230	9		3003
RGQECVEECR	536	10		3004
RGRIHLHGA	432	9		3005
RGRIHLHNGAY	432	10		3006
RGTLQFEDNY	103	10	0.0003	3007
RGTLQFEDNYA	103	11		3008
RILHNGAY	434	8		3009
RILKETELR	713	9	0.0007	3010
RILKETELRK	713	10	0.0570	3011
RIVRGTLQF	100	9		3012
RLLDIDEY	868	10	0.0017	3013
RLLDIDEYH	868	11		3014
RLPASPETH	34	9		3015
RLRIVRGTLQF	98	11		3016
RLVHRDLA	840	8		3017
RLVHRDLAA	840	9		3018
RLVHRDLAAR	840	10	0.1800	3019
RMARDPQR	978	8		3020
RMARDPQRF	978	9	0.0001	3021
RSIRELGSGLA	456	11		3022
RSLTEIK	143	8		3023
RSPLAPSEGA	1072	10		3024
RTVCAGGCA	217	9		3025
RTVCAGGCAR	217	10	0.0068	3026
RVCYGLGMEH	340	10		3027
RVLOGLPR	545	8		3028
RVLOGLPREY	545	10	0.0350	3029
SANIQEFA	358	8		3030
SANIQEFAGCK	358	11		3031
SCTLVCPH	310	9		3032
SCVDLDDK	633	8		3033
SCVTACPY	294	8		3034
SCVTACPYNY	294	10		3035
SDCLACLH	250	8		3036
SDCLACLHF	250	9		3037
SDCLACLHFNH	250	11		3038
SFDGDPASNTA	380	11		3039
SGAFGTVY	728	8		3040

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
SCAFGTYYK	728	9		3041
SCAMPNOA	703	8		3042
SCAMPNOAQMIR	703	11		3043
SGICELHCPA	261	10		3044
SGLALIH	463	8		3045
SGLALIHNTN	463	11		3046
SGVKPDLSY	602	9		3047
SILRRFTH	893	9		3048
SLAFLPESF	373	9		3049
SLPDLSVF	418	8		3050
SLRELGSGLA	457	10		3051
SLRTVCA	214	8		3052
SMPNPEGR	281	8		3053
SMPNPEGRY	281	9	0.0002	3054
SMPNPEGRYTF	281	11		3055
SSEDCOSLTR	208	10	-0.0002	3056
STFKGTPTA	1235	9		3057
STQVCTGTDMK	22	11		3058
SVFONLOVIR	423	10		3059
SVTCFGPEA	573	9	0.0170	3060
TAEDGTQR	323	8		3061
TAEDGTORCEK	323	11		3062
TCSPOPEY	1132	8		3063
TDCCHEQCA	233	9		3064
TDCCHEQCAA	233	10		3065
TDMKRLPA	29	9		3066
TFESMPNPEGR	278	11		3067
TFGASCVTA	290	9		3068
TFKGTPTA	1236	8		3069
TGASPGGLR	130	9		3070
TGPKHSDCLA	245	10		3071
TGTDMLR	27	8		3072
TGTDMLRLPA	27	11		3073
TGPLYISA	407	8		3074
TIDVYMIMVK	948	10	0.0130	3075
TILWKDIF	166	8		3076
TILWKDIFH	166	9		3077
TILWKDIFHK	166	10	0.0430	3078
TLEEITGY	402	8		3079
TLEEITGYLY	402	10	0.0001	3080
TGLEPSEEA	1060	11	0.0004	3081
TLIDTNRSR	182	9		3082
TLIDTNRSA	182	10		3083
TLSPGKNGVVK	1172	11		3084
TSANIQEF	357	8		3085
TSANIQEFA	357	9		3086

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
TVCAGCA	218	8		3087
TVCAGCAR	218	9		3088
TVCAGGCARCK	218	11	0.0004	3089
TVLPSETDGY	1117	11		3090
TPWDQLF	479	8		3091
TPWDQLFR	479	9	0.0006	3092
TVQLVTQLMPY	793	11		3093
TVWELMTF	911	8		3094
TVWELMTFGA	911	10		3095
TVWELMTFGAK	911	11		3096
VACAHYKDPFF	585	11		3097
VACPSGVK	597	9	0.0100	3098
VCAGGCAR	219	8		3099
VCAGGCARCK	219	10		3100
VCPLHNEVTA	314	11		3101
VCTGDMK	25	8		3102
VCTGDMKLR	25	10		3103
VCYGLMEH	341	9		3104
VCYGLGMEHLR	341	11		3105
VDLDDKCCPA	635	10		3106
VFDGLGMGA	1085	10		3107
VFDGLGMGAA	1085	11		3108
VFETLEEITGY	399	11		3109
VFGILKR	670	8		3110
VFGILKRR	670	9		3111
VFQNLQVIR	424	9		3112
VFQNLQVIRGR	424	11		3113
VGGLACH	505	8		3114
VGSCTLVCPLH	308	11		3115
VGSPYVSR	777	8		3116
VIONEDLGPA	988	10		3117
VIRGRILH	430	8		3118
VIRGRILHNGA	430	11		3119
VLGSGAFGTYY	725	11		3120
VLGVVFGILK	666	11		3121
VLIAHQVR	84	9	0.0033	3122
VLIQRNPOLCY	153	11		3123
VLOQLPREY	546	9	0.0012	3124
VLRENTSPK	754	9	0.4000	3125
VLRENTSPKA	754	10		3126
VLKSPNH	851	8		3127
VLKSPNHVK	851	10	0.0820	3128
VMAGVGSPY	773	9	0.0580	3129
VSEFSRMA	973	8		3130
VSEFSRMAR	973	9	-0.0002	3131
VTACPYYNY	296	8		3132

Table XVI
HER2/NEU A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
VTAE DGTQR	322	9	0.0002	3133
VTCTGPEA	574	8		3134
VTGASPGGLR	129	10	0.0002	3135
VTSANIQEF	356	9		3136
VTSANIQEFA	356	10		3137
VTYVELMTF	910	9		3138
VTYVELMTFGA	910	11		3139
VTYNTDTF	272	8		3140
VVFGILIK	669	8		3141
VVFGILIKR	669	9	0.1100	3142
VVFGILIKRR	669	10	0.0030	3143
VVQNEDLGPA	987	11		3144
VVKDVFAF	1180	8		3145
VVKDVFAFGGA	1180	11		3146
VVQNIELTY	55	10	0.0024	3147
VVLGVVF	664	8		3148
WCMQIAKGMYS	825	11		3149
WDQDPPER	1223	8		3150
WDQDPPERGA	1223	10		3151
WDQLFRNPH	482	9		3152
WDQLFRNPHQA	482	11		3153
WPDGENVK	739	9	0.0002	3154
WGLRSLR	452	8		3155
WMALESILR	888	9	-0.0002	3156
WMALESILRR	888	10	0.0085	3157
WMALESILRRR	888	11		3158
WMIDSECR	959	8	-0.0002	3159
WMIDSECRPR	959	10		3160
WMIDSECRPRF	959	11		3161
YGCLLDHVR	803	9		3162
YGLGMEHLR	343	9		3163
YGVTVVELMTF	908	11		3164
YLEDVRLVH	835	9		3165
YLEDVRLVHR	835	10	0.0003	3166
YLPNTASLSF	64	10		3167
YLPQGGGA	1196	8		3168
YLPQGGAA	1196	9		3169
YLPVQQGF	1023	8		3170
YLPVQQGFF	1023	9		3171
YTFGASCYTA	289	10		3172
VVLIHNOVR	83	10	0.0043	3173
YVMAGVGSPI	772	10	0.0100	3174
YVNARHCLPCH	554	11		3175
YVNQPDVR	1139	8		3176

Table XVII
HER2/NEU A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
AAGCTGPK	241	8		3177
AAGCTGPKH	241	9		3178
AAKGLQSLPTH	1094	11		3179
AARNVLVK	847	8		3180
AARPAGATLER	1159	11		3181
ACHPCSPMCK	191	10		3182
ACHQLCAR	510	8		3183
ACHQLCARGH	510	10		3184
ACQPCPNCTH	622	11		3185
ADGKVPK	879	9		3186
ADQVACAH	581	9		3187
ADQVACAHY	581	10		3188
ADQVACAHYK	581	11		3189
AFGGAVENPEY	1186	11		3190
AFSPAFDNL	1212	10	0.0003	3191
AFSPAFDNL	1212	11		3192
AFSPAFDNL	1163	9		3193
AGATLERPK	242	8		3194
AGCTGPKH	221	8		3195
AGGCARCK	1039	8		3196
AGGMVHRH	1039	9		3197
AGGMVHRHR	1039	10		3198
AGVGSPPVSR	775	10		3199
ALESILRR	890	8	0.0006	3200
ALHHNTH	466	9		3201
ALLHTANR	492	8		3202
ALTLDITNR	180	9	0.0005	3203
ALTLDITNRSR	180	11		3204
AMPNQAQMR	705	9		3205
ANIQEFAGCK	359	10	0.0006	3206
ANIQEFAGCKK	359	11		3207
ANKEIDEAY	763	10		3208
ASCVTACPY	293	9	0.0074	3209
ASCVTACPPNY	293	11		3210
ASPEHLDMLR	37	11		3211
ASPLDSTFY	997	9	0.0004	3212
ASPLDSTFYR	997	10	0.0670	3213
CAAGCTGPK	240	9	0.0021	3214
CAAGCTGPKH	240	10		3215
CAGGCARCK	220	9	-0.0002	3216
CLACLFNH	252	9		3217
CLLDHVRENH	805	10	0.0001	3218
CMQIAKMSY	826	10	0.0001	3219
CSKPCARVCY	334	10	0.0002	3220
CSPMCKGSR	195	9	-0.0001	3221
CTGDMKLR	26	9	0.0005	3222
				3223

Table XVII
HER2/NEU A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
CTHSCVDLDDK	630	11		3224
CTIDVYMIMVK	947	11		3225
CTLVCPPLH	311	8		3226
CVACAHYK	584	8		3227
CVARCPGKVK	596	10	0.0042	3228
CVGEGLACH	504	9		3229
CVNCQFLR	528	9	0.0310	3230
CVTACPNY	295	9	0.0004	3231
DCLACLFNH	251	10		3232
DDKCPAEQR	638	10		3233
DGDLGMGAAK	1087	10		3234
DGGKVPK	880	8		3235
DGTORCEK	326	8		3236
DGTORCEKCSK	326	11		3237
DIDETEH	871	8		3238
DIEVQGY	76	8		3239
DLAARNVLVK	845	10	0.0007	3240
DLGMGAAK	1089	8		3241
DILLEKGER	933	8		3242
DLNWCMIQAK	821	11		3243
DSLMIPIWK	607	9	0.0100	3244
DLVDAEY	1016	8		3245
DMGDLVDAEY	1013	11		3246
DSECRPRF	962	9	-0.0002	3247
DTILWKDIFH	165	10		3248
DTILWKDIFHK	165	11		3249
DTNRSRACH	185	9		3250
DVRPQPPSPR	1144	10	0.0001	3251
DVYMIMVK	950	8		3252
EADQCACAH	580	10		3253
EADQCACAHY	580	11		3254
ECRVLQGLPR	543	10		3255
ECVGEGLACH	503	10		3256
EDCSLTR	210	8		3257
EDGTORCEK	325	9		3258
EDVRLVHR	837	8		3259
EFMRMARDPQR	975	11		3260
EGLACHQLCAR	507	11		3261
EGPLPAAR	1154	8		3262
EILKGGVLIQR	147	11		3263
EIPDLLEK	930	8		3264
EIPDLLEKGER	930	11		3265
ELGSLALIH	460	10		3266
ELGSLALHH	460	11		3267
ELHCPALVITY	265	10	0.0002	3268
ELMTFGAK	914	8		3269
ELMTFGAKPY	914	10	0.0002	3270

HER2/NEU A11 Motif Peptides with Binding Data
Table XVII

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
ELVSEFSR	971	8		3271
ELVSEFSRMR	971	11		3272
ENTSPKANK	757	9		3273
ENVKIPVAIK	744	10		3274
ESILRRRFTH	892	10		3275
ESMPNPEGR	280	9	-0.0002	3276
ESMPNPEGRY	280	10	0.0003	3277
ESSEDCQSLTR	207	11		3278
ETELRKVK	717	8		3279
ETEHADGGK	874	10	0.0001	3280
ETHLDMRLR	40	8		3281
ETHLDMRLRH	40	9		3282
ETHLDMRLHLY	40	11		3283
ETLEETIGY	401	9	0.0002	3284
ETLEETIGVLY	401	11		3285
EVQGYVLIH	79	10		3286
EVTAEDEGTQR	321	10	0.0001	3287
FCVARCPGSK	595	11		3288
FDGDLGMGAAK	1086	11		3289
FGASCVTACPY	291	11		3290
FGGAVENPEY	1187	10		3291
FGILIKRR	671	8		3292
FGILIKRQOK	671	11		3293
FLQDIOEVQGY	73	11		3294
FNHSGICELH	258	10		3295
FSPAEDNLY	1213	9	0.0002	3296
FSPAEDNLYY	1213	10	0.0010	3297
FSRMARDPQR	976	10	0.0010	3298
FTHOSDVWSY	899	10	0.0005	3299
GAFGTVYK	729	8		3300
GAGGMVHH	1038	8		3301
GAGGMVHHR	1038	9	0.0043	3302
GAGGMVHHRH	1038	10		3303
GAGGMVHHRHR	1038	11		3304
GAKPYDGIPAR	919	11	0.0041	3305
GAMPNOAQMR	704	10		3306
GAPSTFK	1231	8	0.0001	3307
GASCVTACPY	292	10		3308
GASPGGLR	131	8		3309
GATLERPK	1164	8		3310
GAVENPEY	1189	8		3311
GCLLDHVR	804	8		3312
GCLLDHVRENRR	804	11		3313
GDLGMGAAK	1088	9		3314
GDLVDAEEY	1015	9		3315
GGAAPQPH	1201	8		3316
GGAVENPEY	1188	9	0.0001	3317

Table XVII
HER2/NEU A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
GGLRELQLR	135	9		3318
GGMVHHRH	1040	8		3319
GGMVHHRHR	1040	9		3320
GILIKRROQK	672	10	0.0014	3321
GISWLGLR	449	8		3322
GISWLGLRLSR	449	11		3323
GIWPDGENVK	737	11		3324
GLACHQLCAR	508	10	0.0001	3325
GLALIHNTH	464	10		3326
GLEPSEEEAPR	1062	11		3327
GLGISWLGLR	447	10	0.0001	3328
GLGMEHLR	344	8		3329
GLGMEHLREVR	344	11		3330
GLPREYVNAR	549	10	0.0003	3331
GLPREYVNARH	549	11		3332
GLQSLPTH	1097	8		3333
GLRELQLR	136	8		3334
GMEHLREVR	346	9	-0.0002	3335
GMSYLEDDR	832	9	0.0002	3336
GMVHHRHR	1041	8		3337
GSCTLVCPPLH	309	10	0.0001	3338
GSGAFGTIV	727	9	0.1300	3339
GSGAFGTIVYK	727	10		3340
GSGALIH	462	8		3341
GSLALIH	462	9	0.0022	3342
GTPTAENPEY	1239	10		3343
GTQLFEDNY	104	9	0.0280	3344
GTQRCEKCSK	327	10	0.6100	3345
GVGSPYVSR	776	9	0.0066	3346
GVPDLSY	603	8		3347
GVVFGILIK	668	9	0.0890	3348
GVVFGILIKR	668	10	0.0330	3349
GVVFGILIKRR	668	11		3350
HADGKVPK	878	10	0.0008	3351
HCPALVTY	267	8		3352
HDPSPQOR	1104	8		3353
HDPSPQORY	1104	9		3354
HFNHSGICELH	257	11	0.0002	3355
HLDMRLRLY	42	9		3356
HNQVRQVPQOR	88	11		3357
HNTHLCFVH	470	9		3358
HSCVDLDDK	632	9	0.0007	3359
HSDCLACLIH	249	9		3360
HSICELH	260	8		3361
HTVPWDQLFR	478	10	0.0720	3362
HVKITDFGLAR	858	11		3363
HVRENRR	809	8		3364

Table XVII
HER2/NEU A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
IDSECRPR	961	8		3365
IDSECRPRFR	961	10		3366
IDTNRSRACH	184	10		3367
IDVYMINVK	949	9		3368
ILIKRRQOK	673	9	0.0097	3369
ILIKRRQOKIR	673	11		3370
ILKETELR	714	8		3371
ILKETELRK	714	9	0.0023	3372
ILKETELRKVK	714	11		3373
ILKGGVLIQR	148	10	0.0005	3374
ILRRRFTH	894	8		3375
ILWKDIFH	167	8		3376
ILWKDIFHK	167	9	0.3100	3377
ISWLGRLSLR	450	10	0.0027	3378
ITDFGLAR	861	8		3379
KANKEILDEAY	762	11		3380
KCSKPCAR	333	8		3381
KCSKPCARVCY	333	11		3382
KCWMIDSECR	957	10		3383
KDPPFCVAR	591	9		3384
KGCPAEQR	640	8		3385
KGGVLIQR	150	8		3386
KGQSLPTH	1096	9		3387
KGMSYLEDVLR	831	10		3388
KGPLTDCCH	228	10		3389
KGTPTAENPEY	1238	11		3390
KIPVAIKVLR	747	10	0.0099	3391
KIRKYTMR	681	8	0.0004	3392
KIRKYTMRR	681	9	0.0018	3393
KITDFGLAR	860	9	0.2400	3394
KLRLPASPETH	32	11		3395
KVLRNTSPK	753	10	0.2200	3396
LAARNVLVK	846	9	0.0285	3397
LACHQLCAR	509	9	0.0003	3398
LACHQLCARGH	509	11		3399
LACLFHFNH	253	8		3400
LALIHFNH	465	9	0.0003	3401
LALTLDITNR	179	10	0.0063	3402
LCYODTILWK	161	10		3403
LDDKCGPAEQR	637	11		3404
LDHVRENH	807	8		3405
LDHVRENHGR	807	10		3406
LDIDETEH	870	8		3407
LDIDETEH	870	9		3408
LDMLRHLY	43	8		3409
LFRNPHOALLH	485	11		3410
LGISWLGRLR	448	9		3411

Table XVII
HER2/NEU A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
LGMHLREVR	345	10		3412
LGSGAFCTVY	726	10	0.0003	3413
LGSGAFGTVYK	726	11		3414
LGSLALIH	461	9		3415
LGSLALIIH	461	10		3416
LGVVFGLIK	667	10		3417
LGVVFGLIKR	667	11		3418
LIAHQVR	85	8		3419
LIDTNSR	183	8		3420
LIDTNSRACH	183	11		3421
LIKRRQK	674	8		3422
LIKRRQKIR	674	10	0.0001	3423
LIKRRQKIRK	674	11		3424
LIQNPQLCY	154	10	0.0002	3425
LLDHVRENK	806	9	0.0006	3426
LLDHVRENKGR	806	11		3427
LLDIDETK	869	9	0.0001	3428
LLDIDETKHY	869	10		3429
LLNWCMIQAK	822	10	0.1400	3430
LMPYGCLLDH	800	10		3431
LMTFGAKPY	915	9	0.0003	3432
LNWCMIQAK	823	9	0.0003	3433
LSPGKNGVVK	1173	10		3434
LSVFQNLQVIR	422	11		3435
LSYMPIWK	608	8		3436
LTCSPQPEY	1131	9	0.0061	3437
LTLDITNR	181	8		3438
LTLDITNSR	181	10	0.0005	3439
LVRDLAAR	841	9	0.0014	3440
LKSPNHVK	852	9	0.0700	3441
LVSEFSRMR	972	10	0.0330	3442
LVTQLMPY	796	8		3443
MAGVGSPI	774	8		3444
MAGVGSPIVSR	774	11		3445
MALESILR	889	8		3446
MALESILRR	889	9	0.0237	3447
MALESILRRR	889	10	0.0003	3448
MGDLVDAEY	1014	10	0.0002	3449
MIDSECRPR	960	9	0.0006	3450
MIDSECRPRFR	960	11		3451
MSYLEDVR	833	8		3452
MSYLEDVRLVH	833	11		3453
MITGAKPY	916	8		3454
NARHCLPCH	556	9		3455
NIQEFAGCK	360	9	0.0036	3456
NIQEFAGCKK	360	10	0.0056	3457
NLQVIRGR	427	8		3458

Table XVII
HER2/NEU A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
NLQVIRGRIH	427	11		3459
NTHLCFVH	471	8		3460
NTSPKANK	758	8		3461
NVKIPVAIK	745	9	0.0007	3462
NVLVKSPNH	850	9		3463
NVLKSPNHVK	850	11		3464
PAFDNLY	1215	8		3465
PAFSPAFDNLY	1211	11		3466
PAGATLER	1162	8		3467
PAGATLERPK	1162	10	-0.0002	3468
PAPGAGGMVH	1035	10		3469
PAPGAGGMVHH	1035	11		3470
PAREIPDLLEK	927	11		3471
PASPLDSTFY	996	10	0.0001	3472
PASPLDSTFYR	996	11		3473
PCPINCTH	625	8		3474
PCSPMCKGSR	194	10		3475
PDLLEGER	932	9		3476
PDSLYPEIWK	606	10		3477
PVVRPOPEPR	1143	11		3478
PGAGGMVH	1037	8		3479
PGAGGMVHH	1037	9		3480
PGAGGMVHHRH	1037	10		3481
PGGLRELQLR	134	11		3482
PGKNGVVK	1175	8		3483
PICTIDVY	945	8		3484
PLDSTFYR	999	8		3485
PLPSETDGY	1119	9	0.0002	3486
PLPTDCCH	230	8		3487
PLQRLRIVR	95	9	0.0001	3488
PLTCSQPEY	1130	10	0.0002	3489
PNQAQMRLK	707	10		3490
PSEEEAPR	1065	8		3491
PSGVKPDLSY	601	10	0.0003	3492
PTAENPEY	1241	8		3493
PTHDPSPQOR	1102	10	0.0001	3494
PTHDPSPQORY	1102	11		3495
PVAIKVLR	749	8		3496
PVTGASPGGLR	128	8		3497
QALLHTANR	491	11	0.0010	3498
QAQMRLK	709	9		3499
QCAAGCTGPK	239	8		3500
QCAAGCTGPKH	239	10		3501
QCVACAHY	583	11		3502
QCVACAHYK	583	8		3503
QCVNCSQFLR	527	9		3504
		10		3505

Table XVII
HER2/NEU A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
QDIEVQGY	75	9		3506
QDTILWKDIFH	164	11		3507
QGGAAPQPH	1200	9		3508
QGLGISWGLR	446	11		3509
QGLPREYVNR	548	11		3510
QGNLELY	57	8		3511
QGVYLAH	81	8		3512
QIAGMSY	828	8		3513
QLALTIDTNR	178	11		3514
QLCYQDTILWK	160	11		3515
QLMPYGCILDH	799	11		3516
QLRSLTEILK	141	10	0.0130	3517
QLVTQLMPY	795	9	0.0039	3518
QMRILKETELR	711	11		3519
QNLQVIRGR	426	9		3520
QVCTGTDMK	24	9	0.0520	3521
QVCTGTDMLR	24	11		3522
QVIRGRILH	429	9		3523
QVPLQRLR	93	8		3524
QVPLQRLRIVR	93	11		3525
QVRQVPLQR	90	9	0.0005	3526
QVRQVPLQRLR	90	11		3527
QVQGNLELY	54	11		3528
RACHPCSPMCK	190	11		3529
RCEKCSKPCAR	330	11		3530
RDLAARNVLVK	844	11		3531
RFRELVSFGR	968	11		3532
RFTHQSDVWVS	898	11		3533
RGAPPSTFK	1230	9		3534
RGQECVEECR	536	10		3535
RGRLHNGAY	432	10		3536
RGTLQFEDNY	103	10	0.0015	3537
RILHNGAY	434	8		3538
RILKETELR	713	9	0.0038	3539
RILKETELRK	713	10	0.1100	3540
RLLDIDETEH	868	10	0.0001	3541
RLLDIDETEH	868	11		3542
RLPASPETH	34	9	0.0001	3543
RLVHRDLAAR	840	10		3544
RMARDPQR	978	8		3545
RNPQALLH	487	9		3546
RNVLVKSPNH	849	10		3547
RLSLTEILK	143	8		3548
RTVCAGGCGAR	217	10	0.0130	3549
RVCYGLGMEH	340	10		3550
RVLOGLPR	545	8		3551
RVLOGLPREY	545	10	0.0050	3552

Table XVII
HER2/NEU A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
SANIOEFAGCK	358	11		3553
SCTLVCPHLH	310	9		3554
SCVDLDDK	633	8		3555
SCVTACPY	294	8		3556
SCVTACPYN	294	10		3557
SDCLACLH	250	8		3558
SDCLACLHFNH	250	11		3559
SGAFGTIV	728	8		3560
SGAFGTIVYK	728	9		3561
SGAMPNQAQMR	703	11		3562
SGLALHH	463	8		3563
SGLALHHNTH	463	11		3564
SGVKPDL	602	9		3565
SILRRFTH	893	9		3566
SMPNPEGR	281	8		3567
SMPNPEGRY	281	9	0.0003	3568
SSEDCQSLTR	208	10	0.0020	3569
STQVCTGTDK	22	11		3570
SVFQNLQVIR	423	10	0.0750	3571
TAEDGTOR	323	8		3572
TAEDGTORCEK	323	11		3573
TCSPQPEY	1132	8		3574
TFESMPNPEGR	278	11		3575
TGASPGGLR	130	9		3576
TGTDMLR	27	8		3577
TIDVYMIMVK	948	10	0.1200	3578
TILWKDIFH	166	9		3579
TILWKDIFHK	166	10	3.6000	3580
TLEEITGY	402	8		3581
TLEEITGYLY	402	10	0.0001	3582
TLIDTNRSR	182	9	0.0005	3583
TLSPGKNGVVK	1172	11		3584
TNRSRACH	186	8		3585
TVCAGGCAR	218	9	0.0230	3586
TVCAGGCARCK	218	11		3587
TVPLPSETDGY	1117	11		3588
TVPWDOLFR	479	9	0.0072	3589
TVQLVTQLMPY	793	11		3590
TVWELMTFGAK	911	11		3591
VARCPGVK	597	9	-0.0002	3592
VCAGGCAR	219	8		3593
VCAGGCARCK	219	10		3594
VCTGTDK	25	8		3595
VCTGTDKMLR	25	10		3596
VCYGLGMEH	341	9		3597
VCYGLGMEHLR	341	11		3598
VFLEEITGY	399	11		3599

Table XVII
HER2/NEU A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
VFGLIKR	670	8		3600
VFGLIKRR	670	9		3601
VFQNLQVIR	424	9		3602
VFQNLQVIRGR	424	11		3603
VGEGLACH	505	8		3604
VGSCTLVCPLH	308	11		3605
VGSPYVSR	777	8		3606
VIRGRILH	430	8		3607
VLGSAFGTVY	725	11		3608
VLGVVFGILIK	666	11		3609
VLIHQVR	84	9	0.0007	3610
VLIQNPQLCY	153	11		3611
VLQGLPREY	546	9	0.0002	3612
VLENTSPK	754	9	0.0130	3613
VLKSPNH	851	8		3614
VLKSPNHVK	851	10	0.0072	3615
VMAGVGSPY	773	9	0.0079	3616
VNARHCLPCH	555	10		3617
VNCQFLR	529	8	0.0021	3618
VSEFSMAR	973	9		3619
VTACFPNY	296	8	0.0140	3620
VTAEQGTQR	322	9	0.0005	3621
VTGASPGGLR	129	10		3622
VVFGILIK	669	8	0.7200	3623
VVFGILIKR	669	9	0.0160	3624
VVQGNLELTY	55	10	0.0110	3625
WCMQIAKGMSY	825	11		3626
WDQDPPER	1223	8		3627
WDQFRNPH	482	9		3628
WPDGENVK	739	9	0.0001	3629
WLGLSLR	452	8	-0.0002	3630
WMALESILR	888	10	0.0016	3631
WMALESILRR	888	11		3632
WMALESILRRR	888	12		3633
WMIDSECR	959	8	0.0002	3634
WMIDSECRPR	959	9		3635
YGCLLDHR	803	9		3636
YGLGMEHLR	343	9		3637
YLEDVRLVH	835	9		3638
YLEDVRLVHR	835	10		3639
YVLIHQVR	83	10	0.0001	3640
YVMAGVGSPY	772	10	0.0013	3641
YVNAHCLPCH	554	11	0.0120	3642
YVNPDPVR	1139	8		3643
				3644

Table XVIII
HER2/NEU A24 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
AFDNLVYW	1216	8	0.0039	3645
AFGTVYKGI	730	9	0.0002	3646
AFGTVYKGIW	730	10	0.0010	3647
AFGTVYKGIWI	730	11	0.0008	3648
AFSPAFDNL	1212	9	0.0011	3649
AMPNQAQMRI	705	10	0.0002	3650
AMPNQAQMRIIL	705	11	-0.0003	3651
AWPDSLPL	414	9	0.0041	3652
AYSLTLQGL	440	9	0.1300	3653
AYSLTLQGLGI	440	11	0.0230	3654
CFVHTVPW	475	8	0.0190	3655
CFVHTVPWDQL	475	11	0.0003	3656
CMQIAKGMSYL	826	11	-0.0003	3657
CYGLGMEHL	342	9	0.0180	3658
CYQDTILW	162	8	0.0120	3659
CYQDTILWKDI	162	11	0.0016	3660
DFGLARLL	863	8	0.0005	3661
DFGLARLLDI	863	10	0.0002	3662
EFAGCKKI	363	8	-0.0003	3663
EFAGCKKIF	363	9	0.0003	3664
EYHADGGKVPI	876	11	-0.0003	3665
EYLVPOQGF	1022	9	0.0014	3666
EYLVPOQGF	1022	10	0.0120	3667
EYVNAHCL	553	9	0.0061	3668
GMGAAGKL	1091	8	-0.0003	3669
GMGAAGKLQSL	1091	11	-0.0003	3670
GMSYLEDVRL	832	10	0.0044	3671
GYLISAW	408	8	0.0002	3672
HFHSGICEL	257	10	0.0002	3673
IFGSLAFL	370	8	0.0120	3674
IFHKNNQL	172	8	-0.0003	3675
IFHKNNQLAL	172	10	0.0022	3676
IMVKCWMI	954	8	0.0210	3677
IWPDENVKI	738	11	0.0027	3678
KWMALESI	887	8	0.0080	3679
KWMALESIL	887	8	0.0150	3680
KYTMRRLL	684	8	0.0024	3681
LFEDNYAL	107	8	0.0006	3682
LFEDNYALAVL	107	11	0.0002	3683
LFNPHQAL	485	9	0.0014	3684
LFNPHQALL	485	10	0.0076	3685
LMPYGCLL	800	8	0.0840	3686
LYISAWPDSL	410	10	0.0011	3687
PMCKGSRGW	197	9	0.0005	3688
PYDGIPAREI	922	10	0.0005	3689
PVYSRLGI	780	9	0.1700	3690

Table XV/III
HER2/NEU A24 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
PYVSRLLGICL	780	11	0.0320	3691
QMRILKETEL	711	10		3692
RFRELVSEF	968	9	0.0180	3693
RFTHQSDVW	898	9	0.0110	3694
RFVYQNEIDL	985	10	0.0002	3695
RMARDPQRF	978	9	0.0032	3696
RWGLLLAL	8	8	0.0250	3697
RWGLLLALL	8	9	1.3000	3698
RYSEDPTVPL	1111	10	0.0120	3699
SMNPPEGRYTF	281	11	0.0180	3700
SWLGLRSL	451	8	-0.0003	3701
SWLGLRSLREL	451	11	0.0036	3702
SYGVTWEL	907	9	0.1200	3703
SYLEDVRL	834	8	0.0059	3704
SYMPIWKF	609	8	0.3200	3705
TFGAKPYDGI	917	10	0.0002	3706
TMRRLLQETEL	686	11	-0.0003	3707
TYLPTNASL	63	9	0.0380	3708
TYLPTNASLSF	63	11	8.9000	3709
VFETLEEI	399	8	-0.0003	3710
VFQNLQVI	424	8	-0.0003	3711
VWSYGVTVW	905	9	0.0800	3712
VWSYGVTVWEL	905	11	0.0920	3713
VYIMVVKCW	951	9	0.1600	3714
VYIMVVKCWMII	951	11	1.8000	3715
WMALESIL	888	8	-0.0003	3716
WMIDSECRPRF	959	11	0.0011	3717
YMIMVVKCW	952	8	0.0009	3718
YMIMVVKCWMII	952	10	0.0019	3719

HER2/NEU DR Super Motif Peptides with Binding Data

Table XIX

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wB1	DR2wB2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
YNVLTSDVG	3954	ACPYNVLTSDVGSCT	3720	298								
VIRENTSPK	3955	AIKVLRENTSPKANK	3721	751				0.0075				
LQSLPTHDP	3956	AKGLOSLPTHDPSP	3722	1095								
YDGIPAREI	3957	AKPYDGIPAREIPDL	3723	920			-0.0007	0.3100	-0.0055		-0.0008	
LDIDETEVH	3958	ARLLDIDETEVHADG	3724	867								
VLKSPNHV	3959	ARNVLKSPNHVKIT	3725	848	0.0001	-0.0006						
LTSISAVV	3960	ASPLTSISAVVVGIL	3726	648	0.0890	0.0950	0.0037	0.0010	-0.0025		-0.0005	
LTLOGLIS	3961	AYSLLTLOGLISWLG	3727	440								
MAGVGSPYV	3962	AYVMAGVGSPYVSRL	3728	771								
IFGSLAFLP	3963	CKKIFGSLAFLPEF	3729	367	0.2400	0.0070	0.0016	0.0010	-0.0025		-0.0005	
FNHSGICEL	3964	CLHFNHSGICELHCP	3730	255								
IAKGMSTYLE	3965	CMQIAKGMSTYLEDVR	3731	826								
LVYNTDTF	3966	CPALVTYNTDTFESM	3732	268								
LTRTVCAAG	3967	COSLRTVCAAGCAR	3733	212								
LDKGCFAE	3968	CVDLDDKGCFAEORA	3734	634								
LGMEHLREV	3969	CYGLGMEHLREVRAV	3735	342				0.0083				
YVMAGVGSP	3970	DEAYVMAGVGSPYVS	3736	769	0.0500	0.0029	0.0240	0.0010	0.2300		0.0027	
VGEGLACHQ	3971	DECVGEGLACHQLCA	3737	502								
LGMGAAKGL	3972	DGDLGMGAAGKGLQSL	3738	1087								
VAPLTCSPQ	3973	DGYVAPLTCSPQPEY	3739	1125				-0.0025	-0.0025			
LGLEPSEEE	3974	DLTLGLEPSEEEAPR	3740	1058	0.0010							
LRLPASPET	3975	DMKLRLPASPETHLD	3741	30								
FCVARCPSPG	3976	DPFVCVARCPSPGKVP	3742	592								
FYRSILLEDD	3977	DSTFYRSILLEDDDMG	3743	1001								
LVRDLAAR	3978	DVRLVHRDLAARNVL	3744	838								
MIMVKCMI	3979	DVYMIMVKCMIDSE	3745	950								
VLOGLPREY	3980	ECRVLOGLPREYVNA	3746	543	0.0280	0.0047	0.0042	0.0010	0.0570		0.0220	
YALAVLDNG	3981	EDNYALAVLDNGDPL	3747	109								
LPAARPAGA	3982	EGPLPAARPAGATLE	3748	286								
YTFGASCVT	3983	EGRYTFGASCVTACP	3749	61								
YLPNASLS	3984	ELTYLPNASLSFLQ	3750	892								
LRRRFTQOS	3985	ESILRRRFTQOSDVW	3751	717								
LKKVKVLGS	3986	ETELRKKVKVLGSGAF	3752	693	0.0160	0.0019	0.0052	0.0045	0.0350		0.0061	
LVEPLTPSG	3987	ETELVLEPLTPSGAMP	3753	969	0.0060			0.0710	-0.0025			
LVSEFSRMA	3988	FRELVSSEFSRMAADP	3754	986				-0.0025				
IONEDLGA	3989	FVVIQNEIDLGPASPL	3755	1164								
LERPKTLSP	3990	GATLERPKTLSPGKN	3756	52								
VVOGNLELT	3991	GCOVVOGNLELTLYLP	3757	120								
LNNTPTVTG	3992	GDPLNNTPTVTGASP	3758	506								
LACHOLCAR	3993	GEGLACHOLCARGHC	3759	743								
VKIPVAKV	3994	GENVKIPVAIKVLRE	3760	938	0.0630	0.0047	0.0034	0.0098	-0.0032		-0.0005	
LPQPPICTI	3995	GERLPQPPICTIDVY	3761	881	-0.0005							
VPIKWMAL	3996	GGKVPIKWMALLESIL	3762	151								
LIQNPQLC	3997	GGVLIQNPQLCYQD	3763	518								
WGPGPTQCV	3998	GHCWGPGPTQCVNCS	3764	449								
WLGLRLRE	3999	GISWLGLRLRELGS	3765	464								
LHHNTHLC	4000	GLALHHNTHLCFVH	3766	447								
ISWLGLRL	4001	GLGISWLGLRLREL	3767									

↑
Mound from end
position

HER2/NEU DR Super Motif Peptides with Binding Data

Table XIX

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
YNYLSTDVG	3954	ACPYNYLSTDVGSCT	3720					
VLRENTSPK	3955	AIKVLRENTSPKANK	3721					
LQSLPTHDP	3956	AKGLOSLPTHDPSP	3722					
YDGIPAREI	3957	AKPYDGIPAREIPDL	3723					
LDIDETEH	3958	ARLLDIDETEHADG	3724	-0.0001	-0.0017	-0.0009		
VLKSPNHV	3959	ARNVLKSPNHVKIT	3725	0.0480	0.0350	-0.0004		
LTSISAVV	3960	ASPLTSISAVVGIL	3726					
LTLOGLIS	3961	AYSLLTLOGLISWLG	3727					
MAGVGSPPV	3962	AYVMAGVGSPPVSRL	3728					
IFGSLAFLP	3963	CKKIFGSLAFLPESF	3729	0.0034	0.0270	-0.0004		
FNHSGICEL	3964	CLHFNHSGICELHCP	3730					
IAKGMSTLE	3965	CMQIAKGMSTLEDVR	3731					
LVYNTDTF	3966	CPALVTYNTDTFESM	3732					
LRTVCAGG	3967	CQSLTRTVACGGCAR	3733					
LDDKCPAE	3968	CVDLDDKCPAEQRA	3734					
LGMHLREV	3969	CYGLGMEHLREVRAV	3735					
YVMAGVGS	3970	DEAYVMAGVGSPPVS	3736	0.0020	0.2000	0.0570		
VBEGLACHQ	3971	DECVBEGLACHQLCA	3737					
LGMGAAGL	3972	DGDLGMGAAGLQSL	3738					
VAPLTCSPO	3973	DGYVAPLTCSPOPEY	3739					
LGLPSEEE	3974	DLTLGLEPSEEEAPR	3740					
LRLPASPET	3975	DMKRLRLPASPETHLD	3741		-0.0013			
FCVARCPGS	3976	DPPFCVARCPGSVKP	3742					
FYRSLEDD	3977	DSTFYRSLEDDDDMG	3743					
LVHRDLAAR	3978	DVRLVHRDLAARNVL	3744					
MIMVKCWM	3979	DVYMIMVKCWMIDSE	3745	-0.0003	0.1300	0.0450		
VLQGLPREY	3980	ECRVLQGLPREYVNA	3746					
YALAVLDNG	3981	EDNYALA VLDNGDPL	3747					
LPAARPAGA	3982	EGPLPAARPAGATLE	3748					
YTFGASCVT	3983	EGRYTFGASCVTACP	3749					
YLPTNASLS	3984	ELTYLPTNASLSFLQ	3750					
LRRRFTQHS	3985	ESILRRRFTQSDVV	3751					
LRKVKVLGS	3986	ETELRKVKVLGSGAF	3752	0.0014	0.0380	0.0250		
LVEPLTPSG	3987	ETELVPLTPSGAMP	3753		-0.0013			
LVSEFSRMA	3988	FRELVSFSRMAARDP	3754					
IQNEDLGA	3989	FVVIQNEIDLGPASPL	3755					
LERPKTLSP	3990	GATLERPKTLSPGKN	3756					
VVOGNLELT	3991	GCOVVOGNLELTYP	3757					
LNNITPVGT	3992	GDPLNNTPVGTGASP	3758					
LACHOLCAR	3993	GEGLACHOLCARGHC	3759					
VKIPVAIKV	3994	GENVKIPVAIKVIRE	3760	0.0004	0.0310	0.0010		
LPQPPICTI	3995	GERLPQPPICTIDVY	3761		-0.0011			
VPIKWMAL	3996	GGKVPKWMALLESIL	3762					
LIQRNPQLC	3997	GGVLIQRNPQLCYQD	3763					
WGPPTQCV	3998	GHCWGPPTQCVNCS	3764					
WGLRLSRE	3999	GISWGLRLSRLRELS	3765					
LJHNTLHC	4000	GLALJHNTLHLCFVH	3766					
ISWGLRLSL	4001	GLGISWGLRLSLREL	3767					

↑ moved from core position

Table XIX: HER2/NEU DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wB1	DR2wB2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LALLPPGAA	4002	GLLLALLPPGAASIQ	3768	10								
VFDGLGMG	4003	GSDVFDGDLGMGAAK	3769	1082								
YVSRLLGIC	4004	GSPYVSRLLGICLTS	3770	778					-0.0025			
MKRLRLPASP	4005	GTDMKRLRLPASPETH	3771	28	0.0010							
YKGIWIPDG	4006	GTYYKGIWIPDGENV	3772	732					0.0330			
VWELMTFGA	4007	GVTWVWELMTFGAKPY	3773	909	1.4000							
YISAWPDSL	4008	GYLYISAWPDSLPL	3774	408								
FVHTVPWDO	4009	HLCFVHTVPWDOQLFR	3775	473								
VROVPLORL	4010	HNOVROVPLORLRIV	3776	88								
LAARNVLVK	4011	HRDLAARNVLVKSPN	3777	843								
ICELHCPAL	4012	HSGICELHCPALVTY	3778	260								
ITDFGLARL	4013	HVKITDFGLARLLDI	3779	858								
LHCPALVTY	4014	ICELHCPALVTYNTD	3780	263								
IDVYMIMVK	4015	ICTIDVYMIMVKCWM	3781	946					-0.0032			
LRENTSPKA	4016	IKVLENTSPKANKE	3782	752	-0.0005				0.0400			
MALESILRR	4017	IKWMALESILRRRFT	3783	886	0.9500							
VVLGVVFG	4018	ILLVVVLGVVFGILI	3784	661								
VOGYVLIH	4019	IOEVQGYVLIHQNQV	3785	77								
YTMRRLLQE	4020	IRKTYTMRRLLQETEL	3786	682								
WVGILLVWV	4021	ISAVVVGILLVWVLGV	3787	655								
WPDSLPLDS	4022	ISAWPDSLPLDSVFO	3788	412								
LGLRSLREL	4023	ISWGLRSLRELGSQ	3789	450					-0.0032			
FGLARLLDI	4024	ITDFGLARLLDIDET	3790	861	0.0048							
YLYISAWPD	4025	ITGYLYISAWPDSL	3791	406								
MIDSECRPR	4026	KCWMIDSECRPRFRE	3792	957								
FAFGGAVEN	4027	KDVFAFGGAVENPEY	3793	1182					0.0073			
LDEAYVMAG	4028	KEILDEAYVMAGVGS	3794	765	0.0036		-0.0027					
LPTDCCHEQ	4029	KGPLPTDCCHEQCAA	3795	228					-0.0025			
VAIKVIREN	4030	KIPVAIKVIRENTSP	3796	747	0.0330							
LSYMPIWKF	4031	KPDLSPYMPIWKFDE	3797	605								
VLGSGAFGT	4032	KVKVLGSGAFGTYYK	3798	722								
IKWMALES	4033	KVPKWMALESILRR	3799	883	2.2000	2.7000	2.1000	0.0620	0.0690		0.0073	
LCRWGLLLA	4034	LAALCRWGLLLALLP	3800	3								
LHFNHSGIC	4035	LACLHFNHSGICELH	3801	253								
LPPGAASIQ	4036	LALLPPGAASIQVCT	3802	13								
LDNGDPLNN	4037	LAVLDNGDPLNNTTP	3803	114					-0.0025			
WGLLLALLP	4038	LCRWGLLLALLPPGA	3804	6	0.0940							
VFGILIKRR	4039	LGVVFGILIKRRQOK	3805	667								
LLPPGAAS	4040	LLALLPPGAASQVVC	3806	12								
ICLTSTVOL	4041	LLGICLTSTVOLVTQ	3807	785								
WCMQIAKGM	4042	LLNWCMIQIAKGMSTYL	3808	822	0.8400	0.0057	1.2000	0.0093	0.0011		0.4000	
VVLGVVFGI	4043	LLVVVLGVVFGILIK	3809	662	-0.0008				-0.0025			
LGISWGLR	4044	LQGLISWGLRSLR	3810	445								
LPREYVNR	4045	LQGLPREYVNRHCL	3811	547					-0.0027			
YSEDTPVPL	4046	LQRYSEDTPVPLPSE	3812	1109					0.0270			
LPTHDPSP	4047	LQSLPTHDPSPQRY	3813	1098								
IRGRILNH	4048	LQVIRGRILNHGAYS	3814	428								
LGSLGLIH	4049	LRELGSGLALIHNT	3815	458	0.0310				-0.0025			

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HER2/NEU DR Super Motif Peptides with Binding Data

Table XIX

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LALLPPGAA	4002	GLLLALLPPGAASTQ	3768					
VFDGLGMM	4003	GSDVFDGLGMMGAAG	3769					
YVSRLLGIC	4004	GSPYVSRLLGICLTS	3770		-0.0013			
MKLRLPASP	4005	GTDMKLRLPASPEH	3771					
YKGIWIPDG	4006	GTVMKGIWIPDGENV	3772					
WVLMFTGA	4007	GVTVMELMTFGAKPY	3773		0.0170			
YISAWPDSL	4008	GVL YISAWPDSL PDL	3774					
FVHTVPWDQ	4009	HLCFVHTVPWDQLFR	3775					
VROVPLQRL	4010	HNQVRQVPLQRLRIV	3776					
LAARNVLVK	4011	HRDLAARNVLVKSPN	3777					
ICELHCPAL	4012	HSICELHCPALVTY	3778					
ITDFGLARL	4013	HVKITDFGLARLLDI	3779					
LHCPALVTY	4014	ICELHCPALVTYNTD	3780					
IDVYMIMVK	4015	ICTIDVYMIMVKCWM	3781		-0.0011			
LRENTSPKA	4016	IKVLRNTSPKANKE	3782		0.0040			
MALESILRR	4017	IKWMALESILRRRFT	3783					
VVVLGVVFG	4018	ILLVVVLGVVFGILI	3784					
VQGYVLIAH	4019	IQEVQGYVLIAHNOV	3785					
YTMRLLOE	4020	IRKTYTMRLLOE TEL	3786					
VVGILLVW	4021	ISAVVGIILLVVLGV	3787					
WPDLSLDLS	4022	ISAWPDLSLDLSVFO	3788					
LGLRLREL	4023	ISWGLRLRELQSG	3789					
FGLARLLDI	4024	ITDFGLARLLDIDET	3790		-0.0011			
YLISAWPD	4025	ITGYLYISAWPDSLP	3791					
MIDSECRPR	4026	KCW MIDSECRPRFRE	3792					
FAGGAVEN	4027	KDVFAFGGAVENPEY	3793					
LDEAYVMAG	4028	KEILDEAYVMAGVGS	3794		-0.0011			
LPTDCCHEQ	4029	KGPLPTDCCHEQCAA	3795					
VAIKVLREN	4030	KIPVAIKVLRENTSP	3796		0.0029			
LSYMPIWKF	4031	KPDLSPYMPIWKFDE	3797					
VLGSGAFGT	4032	KVKVLGSGAFGTYYK	3798		0.0190	0.0079		
IKWMALES	4033	KVPKWMALESILRR	3799	0.0031				
LCRWGLLLA	4034	LAALCRWGLLLALLP	3800					
LHFNHSGIC	4035	LACLFHFNHSGICELH	3801					
LPPGAASTQ	4036	LALLPPGAASTQVCT	3802					
LDNGDPLNN	4037	LAVLDNGDPLNNTTP	3803					
WGLLLALLP	4038	LCRWGLLLALLPPGA	3804		0.0021			
VFGILIKRR	4039	LGVVFGILIKRRQOK	3805					
LLPPGAAST	4040	LLALLPPGAASTQVC	3806					
ICLTSTVOL	4041	LLGICLTSTVOLVTQ	3807					
WCMQIAKGM	4042	LLNWCMQIAKGM SYL	3808	0.0390	0.1200	0.4100		
VLGVVFGI	4043	LLVVVLGVVFGILIK	3809		0.0019			
LGISWGLR	4044	LQGLGISWGLRLSLR	3810					
LPREYVNAR	4045	LQGLPREYVNARHCL	3811					
YSEDTPVPL	4046	LQRYSEDTPVPLPSE	3812					
LPTHDPSP	4047	LQSLPTHDPSP LQRY	3813					
IKRILHNG	4048	LQVIRKILHNGAYS	3814					
LGSLGLIH	4049	LRELGSGLALIHNT	3815		-0.0013			

more seen in position

Table XIX HER2/NEU DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w81	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LQRLSLTEI	4050	LRELQLRSLTEILKG	3816	137								
VRVTSANI	4051	LREVRAVTSANIQEF	3817	350								
VRGTQLFED	4052	LRIVRGTLQFEDNYA	3818	99								
VKVLGSGAF	4053	LRKVKVLGSGAFGTV	3819	720								
LRELGSGLA	4054	LSLRELGSGLALIH	3820	455								
FONLQVIRG	4055	LSVFONLQVIRGRIL	3821	422	0.1800	0.0280	0.0740	0.0010	0.0670		0.0100	
ILKGGVLQ	4056	LTEILKGGVLQIRNP	3822	145								
IDTNRSRAC	4057	LTLIDTNRSRACHPC	3823	181								
IISAVVGIL	4058	LTSIISAVVGILLVV	3824	651	0.1900				-0.0025			
LPTNASLSF	4059	LYLYPTNASLSFLQD	3825	62	0.4900	0.0100	0.0560	0.0150	0.3300		0.0041	
WDQDPPERG	4060	LYYWDQDPPERGAPP	3826	1220								
VGSPYVSRL	4061	MAGVSPYVSRLGLI	3827	774								
LREVRAVTS	4062	MEHLREVRAVTSANI	3828	347								
VKCMWIDSE	4063	MIMVKCMWIDSECRP	3829	953								
LKETELRKV	4064	MRILKETELRKVKVL	3830	712								
LEDVRLVHR	4065	MSYLEDVRLVHRDLA	3831	833								
LGPASPLDS	4066	NEDLGPASPLDSTFY	3832	991								
VTFCGPEAD	4067	NGSVTCGPEADQCV	3833	571								
VKDVFAGG	4068	NGVVKDVFAGGAVE	3834	1178								
LTYLPTNAS	4069	NILELTYLPTNASLSF	3835	59	0.4700	0.0280	0.0090	0.0010	0.3800		0.0050	
VIRGRILHN	4070	NLQVIRGRILHNGAY	3836	427								
YWDQDPPER	4071	NLYYWDQDPPERGAP	3837	1219								
LALTLIDTN	4072	NNQLALTLIDTNRSR	3838	176								
LCYQDTILW	4073	NPQLCYQDTILWKDI	3839	158								
LCFVHTVPW	4074	NTHLCFVHTVPWDQL	3840	471								
INCTHSCVD	4075	PCPINCTHSCVDLDD	3841	625								
LPDLSVFQN	4076	PDSLPLDLSVFQNLQV	3842	416								
LQVFETLEE	4077	PEQLQVFETLEEITG	3843	394								
FDGDPASNT	4078	PESFDGDPASNTAPL	3844	378								
VNQPDVRPQ	4079	PEYVNQPDVRPQPPS	3845	1137								
VARCPGVK	4080	PFCVARCPGVKPDLL	3846	594								
LRELQLRSL	4081	PGGLRELQLRSLTEI	3847	134	0.7900				0.0350			
WMALESILR	4082	PIKWMALESILRRRF	3848	885								
VKPDLSYMP	4083	PSGVKPDLSYMPIWK	3849	601								
FKGTPTAEN	4084	PSTFKGTPTAENPEY	3850	1234	-0.0005				-0.0027			
YLSLTDVSGC	4085	PYNYLSLTDVSGCTLV	3851	300								
ILWKDIFHK	4086	ODTILWKDIFHKNNQ	3852	164								
VEECRVLOG	4087	QECVEECRVLQGLPR	3853	538								
FCPDAPGCA	4088	QGFCPDAPGAGGM	3854	1028								
LELYLPTN	4089	QGNLELYLPTNASL	3855	57								
LTLIDTNR	4090	QLALTLIDTNRSRAC	3856	178								
YQDTILWKD	4091	QLCYQDTILWKDIFH	3857	160								
VRPQPPSPR	4092	QPDVRPQPPSPREGP	3858	1142	0.0007							
ICTIDVYMI	4093	QPPICTIDVYMIWK	3859	943	0.0670	0.0540	0.0027	0.0976	-0.0032		0.0046	
FFCPDPAPG	4094	QQGFFCPDPAPGAGG	3860	1027					0.0060			
IRKYTMRL	4095	QQKIRKYTMRLQEQ	3861	679								
VWSYGVTVW	4096	QSDVWSYGVTVWELM	3862	902								
LQRLRIVRG	4097	QVPLQRLRIVRGTLQ	3863	93								

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 end position

HER2/NEU DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LQRLSLTEI	4050	LRELQLRSLTEILKG	3816					
VRAVTSANI	4051	LREVRAVTSANIOEF	3817					
VRGTQLFED	4052	LRVIRGTQLFEDNYA	3818					
VKVLGSGAF	4053	LKRKVKVLGSGAFGTV	3819					
LRELGSLA	4054	LKSLRELGSLALIH	3820					
FQNLQVIRG	4055	LSVFQNLQVIRGRIL	3821	0.0057	0.2900	0.0330		
ILKGGVLIQ	4056	LTEILKGGVLIQIRNP	3822					
IDTNRSRAC	4057	LTLIDTNRSRACHPC	3823					
IISAVVGIL	4058	LTSIISAVVGILLVV	3824		0.0049			
LPTNASLSF	4059	LTYLPTNASLSFLQD	3825	0.0280	0.3200	0.0054		
WDQDPPERG	4060	LYYWDQDPPERGAPP	3826					
VGSPVSRSL	4061	MAGVSPVSRLLGI	3827					
LREVRAVTS	4062	MEHLREVRAVTSANI	3828					
VKCMWIDSE	4063	MIMVKCMWIDSECRP	3829					
LKETELRKV	4064	MRILKETELRKVKVL	3830					
LEDVRLVHR	4065	MSYLEDVRLVHRDLA	3831					
LGPASPLDS	4066	NEDLGPASPLDSTFY	3832					
VTCFGPEAD	4067	NGSVTCFGPEADQCV	3833					
VKDVFAGFG	4068	NGVVKDVFAFGGAVE	3834					
LTYLPTNAS	4069	NLELTYLPTNASLSF	3835	0.0017	0.0680	0.0220		
VIRGRILHN	4070	NLQVIRGRILHNGAY	3836					
YWDQDPPER	4071	NLYWDQDPPERGAP	3837					
LALTLDITN	4072	NNQLALTLDITNRSR	3838					
LCYQDITLW	4073	NPQLCYQDITLWKDI	3839					
LCFVHTVPW	4074	NTHLCFVHTVPWDQL	3840					
INCHSCVD	4075	PCPINCCHSCVDLDD	3841					
LPDLSVFQN	4076	PDSLPLDSVFQNLQV	3842					
LQVFETLEE	4077	PEQLQVFETLEEITG	3843					
FDGDPASNT	4078	PESFDGDPASNTAPL	3844					
VNQPDVRPQ	4079	PEYVNPQDVRPQPPS	3845					
VARCPGKVK	4080	PFCVARCPGKVKPDL	3846					
LRELQLRSL	4081	PGGLRELQLRSLTEI	3847					
WMALESILR	4082	PIKWMALESILRRRF	3848		0.0078			
VKPDLSYMP	4083	PSGVKPDLSYMPIWK	3849		-0.0011			
FKGTPTAEN	4084	PSTFKGTPTAENPEY	3850					
YLSTDVGS	4085	PYNVYSTDVGSCTLV	3851					
ILWKDIFHK	4086	ODTILWKDIFHKNNQ	3852					
VEECRVLOG	4087	QECVEECRVLQGLPR	3853					
FCPDPAPGA	4088	QGFCCPDPAPGAGGM	3854					
LELTYPN	4089	QGNLELTYPNLSL	3855					
LTLIDTNR	4090	QLALTIDTNRSRAC	3856					
YQDTILWKD	4091	OLCYQDTILWKDIFH	3857					
VRPQPSPR	4092	QPDYRQPQPSPREGP	3858		-0.0011			
ICTIDVYMI	4093	OPPICTIDVYMIWK	3859	0.0013	0.1000	0.0051		
FFCPDPAPG	4094	QQGFFCPDPAPGAGG	3860					
IRKYTMRL	4095	QQKIRKYTMRLLOE	3861					
VWSYGVTVV	4096	QSDVWSYGVTVVWELM	3862					
LQRLRVRG	4097	QVPLQRLRVRGTQL	3863					

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Table XIX HER2/NEU DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w81	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VNARHCLPC	4098	REYNARHCLPCHE	3864	552								
ILNHGAYSL	4099	RGRIHNGAYSLTQ	3865	432								
LGSDLLNW	4100	RGRLGSDLLNWCMIQ	3866	814								
YQGVVQVQ	4101	RHLYQGVVQVQGNLE	3867	47								
FRELVEFS	4102	RPRFRELVEFSRMA	3868	966								
LQETELVEP	4103	RRLQETELVEPLTP	3869	688								
LEDDMDGL	4104	RSLLDDMDGLVDA	3870	1006								
LLALLPPG	4105	RWGLLLALLPPGAAS	3871	8	12.0000	0.1300	0.0270	0.0080	0.2800		0.0710	
FGASCVTAC	4106	RYTFGASCVTACPN	3872	288				0.0010				
VGILLVVVL	4107	SAVVGILLVVVLGVV	3873	656								
WSYGVTVWE	4108	SDVWSYGVTVWELMT	3874	903								
LOGLISWL	4109	SLTLOGLISWLGLR	3875	442								
LLNWCMIQ	4110	SQDLLNWCMIQAKGM	3876	819								
LRQECVEE	4111	SQFLRQECVEECRV	3877	532								
LGICLTSTV	4112	SRLLGICLTSTVQLV	3878	783								
VGSCITLVC	4113	STDVGSCTLVCPPLHN	3879	305	0.3500	0.0220	-0.0007	0.0062	0.1200		0.0140	
VTVWELMTF	4114	SYGVTWELMTFEGAK	3880	907								
LOPEQLQVF	4115	TAPLQPEQLQVFETL	3881	389				0.0023	-0.0032			
YVAPLTCSF	4116	TDGYYAPLTCSQPE	3882	1124	-0.0005							
LKGGVLIQR	4117	TEILKGGVLIQRNPQ	3883	146								
VEPLTPSGA	4118	TELVEPLTPSGAMPN	3884	694								
YVMIMVKCW	4119	TIDVYIMIMVKCWMID	3885	948								
FEDNYALAV	4120	TQLFEDNYALAVLDN	3886	105	0.0530				-0.0025			
MPYGCCLDH	4121	TQLMPYGCCLDHVRE	3887	798								
VCAGGCARC	4122	TRTVAGGCARCCKGP	3888	216								
VTGASPGGL	4123	TRTVGASPGGLREL	3889	126								
LVTLQMPYG	4124	TVQLVTQMPYGCLL	3890	793	0.2300	0.7500	0.0009	0.0010	0.0460		-0.0005	
LHNOEVTAE	4125	VCPLHNOEVTAEDET	3891	314	-0.0004				-0.0025			
LTPSGAMPN	4126	VEPLTPSGAMPNQAQ	3892	697	-0.0008				-0.0025			
LLVVVLGVV	4127	VGILLVVVLGVVFGI	3893	659								
VPWDQLFRN	4128	VHTVPWDQLFRNPHQ	3894	477	0.0700	0.0110	0.0620	0.0220	0.0021		0.4700	
VVFGILIKR	4129	VLGVVFGILIKRRQQ	3895	666								
VTQLMPYGC	4130	VQLVTQLMPYGCCLLD	3896	794								
VTSANIQEF	4131	VRAVTSANIQEFAGC	3897	353								
VHRDLAARN	4132	VRLVHRDLAARNVLV	3898	839								
VPLQRLRIV	4133	VROVPLQRLRIVRGT	3899	91	0.0340	0.0064	0.0033	0.3400	0.0150		0.2700	
LLGICLTST	4134	VSRLGICLTSTVQL	3900	782								
LMPYGCCLLD	4135	VTQLMPYGCCLLDHVR	3901	797								
ILLVVVLGV	4136	VVGILLVVVLGVVFG	3902	658								
LMTFGAKPY	4137	VWELMTFGAKPYDGI	3903	912	-0.0004	0.0990	0.1000	0.0010	-0.0025		0.0054	
LLALLPPGA	4138	WGILLALLPPGAAST	3904	9	0.0870	0.2100	0.0110	0.0013	0.0550		0.2500	
IPAREIPDL	4139	YDGIPAREIPDLLEK	3905	923	5.1000				1.3000			
MVKCWMIDS	4140	YMMVKCWMIDSECR	3906	952								
IAHQVRQV	4141	YVIAHQVRQVRPLQ	3907	83								

monoclonal antibody

HER2/NEU DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR7	DR8w2	DR9	DRw53
VNARHCLPC	4098	REYVNARHCLPCHE	3864				
ILHNGAYSL	4099	RGRILHNGAYSLTQ	3865				
LGSQDLN	4100	RGRLSQDLNLCMQ	3866				
YQCCVVG	4101	RHLVQCCVVGQNL	3867				
FRELVSF	4102	RPRFRELVSFGRMA	3868				
LOETELVEP	4103	RRLLOETELVEPLTP	3869				
LEDDMDGL	4104	RSLEDDMDGLVDA	3870				
LLALLPPG	4105	RWGLLLALLPPGAAS	3871	-0.0013	0.1200		
FGASCYTAC	4106	RYTFGASCYTACPN	3872				
VGILLVVL	4107	SAVVGILLVVLGVV	3873				
WSYGVTVWE	4108	SDWSYGVTVWELMT	3874				
LOGLGISWL	4109	SLTLQGLGISWLGLR	3875				
LLNWCMIQIA	4110	SQDLLNWCMIQAKGM	3876				
LRQCEVEE	4111	SQFLRQCEVEECRV	3877				
LGICLTSTV	4112	SRLLGICLTSTVQLV	3878	0.5600	0.0009		
VGSCTLVCP	4113	STDVGSCTLVCPHNL	3879				
VTWVWELMTF	4114	SYGVTWVWELMTFGAK	3880				
LQPEQLQVF	4115	TAPLQPEQLQVFETL	3881	-0.0011			
YVAPLTCSP	4116	TDGYVAPLTCSPQPE	3882				
LKGGVLIQR	4117	TEILKGGVLIQRNPQ	3883				
VEPLTPSGA	4118	TELVEPLTPSGAMPN	3884				
VYIMIMKVCW	4119	TIDVYIMIMKVCWMID	3885				
FEDNYALAV	4120	TQLFEDNYALAVLDN	3886	0.0160			
MPYGCCLLDH	4121	TQLMPYGCCLLDHVRE	3887				
VCAGGCARC	4122	TRTVCAGGCARCCKGP	3888				
VTGASPGGL	4123	TPVTGASPGGLREL	3889				
LVTLQMPYG	4124	TVQLVTQMPYGCCLL	3890	0.0031	0.0069		
LHNOEVTAE	4125	VCPLHNOEVTAEEDGT	3891	0.0100			
LTPSGAMPN	4126	VEPLTPSGAMPNQAQ	3892	-0.0013			
LLVVVLGVV	4127	VGILLVVVLGVVFGI	3893	-0.0011			
VPWDQLFRN	4128	VHTVPWDQLFRNPHQ	3894				
VVEGILIKR	4129	VLGVVFGILIKRRQ	3895	0.0320	0.6400		
VTQLMPYGC	4130	VQLVTQLMPYGCCLD	3896				
VTSANIOEF	4131	VRAVTSANIOEFAGC	3897				
VHRDLAARN	4132	VRLVHRDLAARNVLV	3898	0.0230	0.1000		
VPLQRLRIV	4133	VRQVPLQRLRIVRGT	3899				
LLGICLTST	4134	VSRLLGICLTSTVQL	3900				
LMPYGCCLLD	4135	VTQLMPYGCCLLDHVR	3901				
ILLVVVLGV	4136	VVGILLVVVLGVVFG	3902	-0.0013			
LMTFGAKPY	4137	VWELMTFGAKPYDGI	3903	0.0089	0.4500		
LLALLPPGA	4138	WGLLLALLPPGAAST	3904	-0.0013			
IPAREIPDL	4139	YDGIPAREIPDLLEK	3905				
MVKCWMIDS	4140	YMIMVKCWMIDSECR	3906				
IAHNQVRQV	4141	YVLIAHNQVRQVPLQ	3907				

moved from
end position

HER2/NEU DR 3a Motif Peptides with Binding Data

Table XXa

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DRI	DR2w281	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VIRENTSPK	4142	AIKVLRENTSPKANK	3908	751				0.0075				
LDIDETEVH	4143	ARLLDIDETEVHADG	3909	867	0.0001	-0.0006	-0.0007	0.3100	-0.0055		-0.0008	
LGMEHLREV	4144	CYGLGMEHLREVRAV	3910	342				0.0083				
LGLESEEE	4145	DLTLGLEPSEEEAPR	3911	1058				-0.0025				
YYWDQDPE	4146	DNLYYWDQDPPERGA	3912	1218				-0.0025				
LWKDFHKN	4147	DTILWKDFHKNQQL	3913	165				-0.0027				
YHADGKVP	4148	ETEHADGKVKPIKW	3914	874				-0.0027				
LYSEFSRMA	4149	FRELVSFSRMAIDP	3915	969				0.0710				
MARDPQRFV	4150	FSRMAIDPQRFVVIQ	3916	976				0.1600				
IQNEDLGA	4151	FVVIQNEIDLGPASP	3917	986				-0.0025				
VDAEEYLVP	4152	GDLVDAEEYLVPQQG	3918	1015				0.0250				
LPEDNYALA	4153	GTQLFEDNYALAVLD	3919	104	0.9500			0.2200	0.0400			
MALESILRR	4154	IKWMALESILRRRFT	3920	886				-0.0027				
FPDEGACQ	4155	IWKFPDEGACQPCP	3921	613				-0.0027				
LPTDCHEQ	4156	KGPLPTDCHEQCAA	3922	228				-0.0025				
VVKDVFAFG	4157	KNGVVKDVFAFGGAV	3923	1177				-0.0027				
LPREYVNAH	4158	LQGLPREYVNAHCL	3924	547				0.0270				
YSEDPTVPL	4159	LQRYSEDPTVPLPSE	3925	1109				-0.0027				
YNTDTFESM	4160	LVTYNTDTFESMPNP	3926	271				-0.0027				
LLQETELVE	4161	MRRLQETELVEPLT	3927	687				-0.0027				
ILDEAYVMA	4162	NKEILDEAYVMAGVG	3928	764				0.0047				
VTAEADGTQR	4163	NOEVTAEADGTQCEK	3929	319				-0.0027				
FDGDPASNT	4164	PESFDGDPASNTAPL	3930	378				-0.0027				
VKPDLSYMP	4165	PSGVKPDLSYMPIWK	3931	601				-0.0027				
FCPPDPAPGA	4166	QGFPPDPAPGAGGM	3932	1028	-0.0005	0.0150	0.5900	0.3200	0.0230		0.0041	
ILKETELRK	4167	QMRILKETELRKVKV	3933	711	0.0419			0.0080	-0.0055			
LEDDDMGDL	4168	RSLEDDDMGDLVDA	3934	1006				-0.0025				
FDGDLGMA	4169	SDVFDGDLGMAAKG	3935	1083				-0.0027				
FLPESFDGD	4170	SLAFLEPESFDGDPAS	3936	373				0.0520				
FLQIQEVQ	4171	SLFLQIQIEVQGYV	3937	70				0.0023				
LQPEQLQVF	4172	TAPLQPEQLQVFETL	3938	389				-0.0025				
LPSETDGYV	4173	TVPLPSETDGYVAPL	3939	1117				0.0023				
VPWDQLFRN	4174	VHTVPWDQLFRNPHQ	3940	477				0.0220	0.0150			
VHRDLAARN	4175	VRLVHRDLAARNVLV	3941	839	0.0340	0.0064	0.0033	0.3400			0.2700	
FGPEADQCV	4176	VTCFGEADQCVACA	3942	574				-0.0027				
LSTDVGSCT	4177	YNLSTDVGSCTLYC	3943	301				0.0059				
LLEDDDMGD	4178	YRSILLEDDDMGDLVD	3944	1005				0.0630				

↑ moved from end position

Table XXa HER2/NEU DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VLRENTSPK	4142	AIKVLRENTSPKANK	3908					
LDIDETEH	4143	ARLLDIDETEHADG	3909					
LGMEHLREV	4144	CYGLGMEHLREVRAV	3910	-0.0001	-0.0017	-0.0009		
LGLEPSEE	4145	DLTLGLEPSEEEAPR	3911					
YVWDQDPE	4146	DNLVYWDQDPPPERGA	3912					
LWKDFHKN	4147	DTILWKDFHKNQOL	3913					
YHADGKVP	4148	ETETHADGKVPKIKW	3914					
LVSEFSRMA	4149	FRELVSFSESRMARDP	3915					
MARDPQRFV	4150	FSRMARDPQRFVVIQ	3916					
IONEDLQPA	4151	FVVIQNEIDLGPASPL	3917					
VDAEYLVP	4152	GDLVDAEYLVPOQG	3918					
LFEDNYALA	4153	GTQLFEDNYALAVLD	3919					
MALESILRR	4154	IKVMALESILRRRFT	3920					
FPDEEGACQ	4155	IWKFPDEEGACQPCP	3921					
LPTDCCHEQ	4156	KGPLPTDCCHEQCAA	3922					
VKDVFAFG	4157	KNGVVKDVFAFGGAV	3923		0.0040			
LPREYVNR	4158	LOGLPREYVNRHCL	3924					
YSEDTPVPL	4159	LQRYSEDTPVPLPSE	3925					
YNTDTFESM	4160	LVTYNTDTFESMPNP	3926					
LLQETELVE	4161	MRRLLQETELVEPLT	3927					
ILDEAYYMA	4162	NKEILDEAYYMAVG	3928					
VTAEQGTQR	4163	NOEVTAEQGTQCEK	3929					
FDGDPASNT	4164	PESFGDPASNTAPL	3930					
VKPDLSYMP	4165	PSGVKPDLSYMPIWK	3931					
FCPDAPGA	4166	QGFCFPDAPGAGGM	3932	-0.0011	-0.0130	0.0064		
ILKETELRK	4167	QMRILKETELRKVKV	3933	0.0008				
LEDDDMGDL	4168	RSLLLEDDDMGDLVDA	3934					
FDGDLGMGA	4169	SDVFDGDLGMGAAG	3935					
FLPESFDGD	4170	SLAFLPESFDGDPAS	3936					
FLQDIQEVQ	4171	SLSFLQDIQEVQGYV	3937					
LQPEQLQVF	4172	TAPLQPEQLQVFETL	3938					
LPSETDGYV	4173	TVPLPSETDGYVAPL	3939					
VVWDQLFRN	4174	VHTVWDQLFRNPHQ	3940					
VHRDLAARN	4175	VRLVHRDLAARNVLV	3941	0.0430	0.0230	0.1000		
FGPEADQCV	4176	VTCFGPEADQCVACA	3942					
LSTDVGSCT	4177	YNLSSTDVGSCTLVC	3943					
LLEDDDMGD	4178	YRSLLLEDDDMGDLVD	3944					

↑
moved from
end
position

Table XXb HER2/NEU DR 3b Motif Peptides with Binding Data

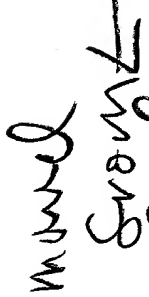

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LIDNRSRA	4179	ALTLIDTNRSRACHP	3945	180				0.0350				
IDSECRPF	4180	CWMIDSECRPFREL	3946	958	0.0036	-0.0006	0.0150	0.4500	-0.0055		-0.0008	
YLEDVRLVH	4181	GMSYLEDVRLVHRDL	3947	832				0.1800				
VDLDDKGGP	4182	HSCVDLDDKGGCPAEQ	3948	632				-0.0027				
IHHNTHLCF	4183	LALIHNTHLCFVHT	3949	465	0.0140	0.0990	0.0009	0.3100	-0.0055		0.0025	
AAPQPHPPP	4184	QGGAAPQPHPPPAFS	3950	1200				-0.0025				
ASPETHLDM	4185	RLPASPEHLDMLRH	3951	34				-0.0027				
AHNQVRQVP	4186	VLIAHNQVRQVPLOP	3952	84				0.0290				
LFRNPHQAL	4187	WDQLFRNPHQALLHT	3953	482	-0.0001	0.0015	-0.0007	0.9000	-0.0055		-0.0008	

91 moved from end position

added

Table XXb HER2/NEU DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LIDTNRSA	4179	ALTLDITNRSRACHIP	3945					
IDSECRPRF	4180	CWMIDSECRPRFREL	3946	-0.0001	-0.0014	0.0028		
YLEDVRLVH	4181	GMSYLEDVRLVHRDL	3947					
VLDLKGCP	4182	HSCVDLDDKGCFAEQ	3948					
IHNTHLCF	4183	LALIHNTHLFCFVHT	3949	0.7500	0.0200	0.0330		
AAPQHPPP	4184	QGGAAPOPHPPPAFS	3950					
ASPETHLDM	4185	RLPASPETHLDMLRH	3951					
AHNQVRQVP	4186	VLIAHNQVRQVPQOR	3952					
LFRNPQAL	4187	WDQLFRNPQALLHT	3953	0.0410	-0.0017	-0.0009		

 mutated
 position

 added

Table XXII. A2 supermotif analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
Her2/neu.5	9	ALCRWGILL	4227	100	--	278	--	--	2
Her2/neu.5B3V9	9	ALBRWGILLV	4228	18	33	4.2	285	--	4
Her2/neu.5M2B3V9	9	AMBRWGILLV	4229	36	473	16	726	--	3
Her2/neu.153	9	VLIQRNPQL	4230	23	3909	3.3	1057	--	2
Her2/neu.153V9	9	VLIQRNPQV	4231	55	768	135	385	--	3
Her2/neu.369	9	KIFGSLAFL	4232	36	9.0	19	23	3333	4
Her2/neu.369V2V9	9	KVFGSLAFV	4233	20	19.0	769	15	29	4
Her2/neu.369T2V9	9	KTFGSLAFV	4234	35	13.0	1010	14	17	4
Her2/neu.369L2V9	9	KLFGSLAFV	4235	5.8	7.5	19	17	1270	4
Her2/neu.653	9	SIISAVVGI	4236	69	524	35	285	148	4
Her2/neu.653.L2V9	9	SLISAVVGV	4237	7.1	10	16	20	110	5
Her2/neu.665	9	VVLGVVFGI	4238	14	--	2500	430	2000	2
Her2/neu.665V2V9	9	VVLGVVFGV	4239						
Her2/neu.665L2V9	9	VLLGVVFGV	4240	2.4	17	14	6.0	8000	4
Her2/neu.952	10	YMIMVKCWMV	4241	20	307	83	116	267	5
Her2/neu.952L2V10	10	YLIMVKCWMV	4242	13	56	116	18	84	5
Her2/neu.952L2B7V10	10	YLIMVKBWMV	4243	7.2	66	77	11	851	4

-- indicates binding affinity = 10,000nM.

Table XXII A01A Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0101 nM
52.0013	8	VTACPYN	4244	Her2/neu.296	250
52.0118	11	ETHLDMLRHLY	4245	Her2/neu.40	89.3
52.0121	11	ASCVTACPYN	4246	Her2/neu.293	131.6
52.0124	11	ETLEEITGYLY	4247	Her2/neu.401	56.8
52.0125	11	EADQCVACAHY	4248	Her2/neu.580	250
57.0016	9	HTDMLRHLY	4249	Her2/neu.42.T2	1.9
57.0017	9	GTDLFEDNY	4250	Her2/neu.104.D3	0.9
57.0018	9	ATCVTACPY	4251	Her2/neu.293.T2	49
57.0019	9	ETDEEITGY	4252	Her2/neu.401.D3	16.7
57.0022	9	VMDGVGSPY	4253	Her2/neu.773.D3	39.7
57.0023	9	LTDIDET	4254	Her2/neu.869.T2	5.7
57.0024	9	ATPLDSTFY	4255	Her2/neu.997.T2	36.2
57.0025	9	LTDSPQPEY	4256	Her2/neu.1131.D3	31.6
57.0027	9	FTPAFDNLY	4257	Her2/neu.1213.T2	7.8
57.0028	9	SPDFDNLYY	4258	Her2/neu.1214.D3	73.5
57.0107	10	GTDMKLRLPY	4259	Her2/neu.28.Y10	50
57.0109	10	PTDCCHEQCY	4260	Her2/neu.232.Y10	46.3
57.011	10	PTDCCHEQCA	4261	Her2/neu.232	125
57.0111	10	ETMPNPEGRY	4262	Her2/neu.280.T2	3.9
57.0112	10	TLDEITGYLY	4263	Her2/neu.402.D3	3.4
57.0113	10	CTQIAKGMSY	4264	Her2/neu.826.T2	19.2
57.0114	10	FTDQSDVWSY	4265	Her2/neu.899.D3	0.6
57.0115	10	PADPLDSTFY	4266	Her2/neu.996.D3	19.2
57.0116	10	MTDLVDAEEY	4267	Her2/neu.1014.T2	2.3
57.0117	10	FTPAFDNLYY	4268	Her2/neu.1213.T2	0.8
57.0118	10	GTDTAENPEY	4269	Her2/neu.1239.D3	25.8
57.0129	11	PTDCCHEQCAY	4270	Her2/neu.232.Y11	17.9
57.013	11	PTDCCHEQCAA	4271	Her2/neu.232	58.1

added

Table XXII B A03 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3 XRN
1371.34	10	IVKGGVLIQR	4272	Her2/neu.148.V2	275	7500	72	126.1	28.6	4
1371.35	10	IVKGGVLIQK	4273	Her2/neu.148.V2K10	26.2	101.7	450	6590.9	26.7	4
1371.36	10	TVLWKDIFHK	4274	Her2/neu.166.V2	733.3	40	9000	5686.3	470.6	2
1371.37	10	TVLWKDIFHR	4275	Her2/neu.166.V2R10	8461.5	285.7	600	76.3	42.1	3
1371.38	9	IVWKDIFHK	4276	Her2/neu.167.V2	23.4	40	246.6	852.9	177.8	4
1371.39	9	IVWKDIFHR	4277	Her2/neu.167.V2R9	142.9	285.7	6	16.1	15.4	5
1371.4	9	TVBAGGBAR	4278	Her2/neu.218.B3B7	314.3	111.1	246.6	241.7	8	5
1371.41	9	TVBAGGBAK	4279	Her2/neu.218.B3B7K9	23.9	28.6	45000	36250	7.3	3
1371.42	10	IVWLGLRSLR	4280	Her2/neu.450.V2	234	1935.5	11.3	193.3	7.3	4
1371.43	10	IVWLGLRSLK	4281	Her2/neu.450.V2K10	3.9	127.7	272.7	2071.4	11.6	4
1371.44	10	HVVPWDQLFR	4282	Her2/neu.478.V2	7333.3	1333.3	391.3	193.3	3.6	3
1371.45	10	HVVPWDQLFK	4283	Her2/neu.478.V2K10	180.3	375	-60000	36250	8.9	3
1371.46	9	BVNBSQFLR	4284	Her2/neu.528.B1B4	177.4	80	37.5	58	9.9	5
1371.47	9	BVNBSQFLK	4285	Her2/neu.528.B1B4K9	34.4	22.2	60	4264.7	14.5	4
1371.48	9	VVFGILIKK	4286	Her2/neu.669.K9	21.6	19.4	3750	10000	34.8	3
1371.49	9	VVRENTSPK	4287	Her2/neu.754.V2	68.8	333.3	750	1208.3	3478.3	2
1371.5	9	VVRENTSPR	4288	Her2/neu.754.V2R9	200	5454.5	375	126.1	177.8	4
1371.52	9	LVDHVRENK	4289	Her2/neu.806.V2K9	297.3	722.9	-60000	-58000	2580.6	1
1371.53	9	LVARNVLVK	4290	Her2/neu.846.V2	42.3	214.3	9000	-58000	205.1	3
1371.54	9	LVARNVLVR	4291	Her2/neu.846.V2R9	261.9	3157.9	9000	19333.3	26.7	2
1371.55	9	LKSPNHVR	4292	Her2/neu.852.R9	7857.1	12000	197.8	107.4	50	3
1371.56	9	KVTDGFLAR	4293	Her2/neu.860.V2	200.7	75.9	105.9	-58000	133.3	4
1371.57	9	KVTDGFLAK	4294	Her2/neu.860.V2K9	36.7	46.2	3461.5	-58000	816.3	2
1371.58	9	MVLESILRR	4295	Her2/neu.889.V2	215.7	272.7	206.9	152.6	22.2	5
1371.59	9	MVLESILRK	4296	Her2/neu.889.V2K9	61.1	16.2	20000	2636.4	381	3
1371.6	10	LVSEFSRMAK	4297	Her2/neu.972.K10	250	71.4	2250	5272.7	61.5	3
1371.61	10	AVPLDSTFYR	4298	Her2/neu.997.V2	-110000	88.2	30000	2636.4	72.7	2
1371.62	10	AVPLDSTFYK	4299	Her2/neu.997.V2K10	550	33.3	1500	22307.7	228.6	2

added

Table XXIIIC A02 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO.	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 XRN
1382.01	9	ATCRWGGLLV	4300	Her2/neu.5.T2V9	-50000	21500	4347.8	-37000	40000	0
1382.02	9	AVCRWGGLLV	4301	Her2/neu.5.V2V9	-50000	6142.9	2631.6	18500	26666.7	0
1382.03	9	ATBRWGGLLV	4302	Her2/neu.5.T2B3V9	16666.7	215	322.6	2176.5	1739.1	2
1382.04	9	AVBRWGGLLV	4303	Her2/neu.5.V2B3V9	10000	215	140.8	2176.5	4705.9	2
1390.01	9	ALBRWGGLLV	4304	Her2/neu.5.B3	238.1	0.6	11.6	6166.7	7272.7	3

✓ added

Table XXIID A24 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*2401 nM</u>
52.0045	8	RWGLLLAL	4305	Her2/neu.8	480
52.0056	8	SYMPIWKF	4306	Her2/neu.609	37.5
52.0148	11	TYLPTNASLSF	4307	Her2/neu.63	1.3
52.0159	11	PYVSRLLGICL	4308	Her2/neu.780.	375
52.0162	11	VWSYGVTWEL	4309	Her2/neu.905	130.4
52.0163	11	VYMIMVKCWM	4310	Her2/neu.951	6.7
57.0046	9	RYGLLLALF	4311	Her2/neu.8.Y2F9	1.3
57.0047	9	TYLPTNASF	4312	Her2/neu.63.F9	44.4
57.0048	9	CYGLGMEHF	4313	Her2/neu.342.F9	164.4
57.0049	9	AYPDSLPDF	4314	Her2/neu.414.Y2F9	23.5
57.005	9	AYSLTLQGF	4315	Her2/neu.440.F9	52.2
57.0051	9	EYVNARHCF	4316	Her2/neu.553.F9	150
57.0052	9	PYVSRLLG	4317	Her2/neu.780.F9	9.2
57.0053	9	KYMALESIF	4318	Her2/neu.887.Y2F9	19
57.0054	9	RYTHQSDVF	4319	Her2/neu.898.Y2F9	60
57.0055	9	VYSYGVTVF	4320	Her2/neu.905.Y2F9	16.2
57.0056	9	SYGVTWVEF	4321	Her2/neu.907.F9	26.1
57.0057	9	VYMIMVKCF	4322	Her2/neu.951.F9	19
57.0058	9	RYRELVSEF	4323	Her2/neu.968.Y2	36.4
57.0059	9	RYARDPQRF	4324	Her2/neu.978.Y2	120
57.008	10	LYISAWPDSF	4325	Her2/neu.410.F10	10
57.0082	10	GYSYLEDVRF	4326	Her2/neu.832.Y2F10	235.3

added

Table XXIII B07 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO.	Source	B*0702 nM	B*3501 nM	B*5101 nM	B*5301 nM	B*5401 nM	B7 XRN
48.0027	8	FPKANKEA	4327	HER2/neu.760F118	0.16	-36000	2500	-93000	3125	1

4327

added

Table XXIII. Immunogenicity A2 peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide ¹	CTL Wild-type ¹	CTL Tumor ¹
Her2/neu.5	9	ALCRWGGLL	4328	100	-- ²	278	--	--	2		2/2	2/2
Her2/neu.48	9	HL YQGCQVV	4329	139	307	13	514	1143	3		1/2	0/2
Her2/neu.106	9	QLFEDNYAL	4330	17	226	11	463	2105	4		0/2	0/2
Her2/neu.106	10	QLFEDNYALA	4331	357	662	9.1	218	74	4		0/2	0/2
Her2/neu.369	9	KIFGSLAFL	4332	36	9.0	19	23	3333	4		6/7	4/7
Her2/neu.435	9	ILHNGAYSL	4333	75	358	100	569	--	3		3/3	1/3
Her2/neu.653	9	SIISAVVGI	4334	69	524	35	285	148	4		0/3	
Her2/neu.773	10	VMAGVGSPYV	4335	200	391	13	3700	--	3		1/2	0/2
Her2/neu.789	9	CLTSTVQLV	4336	208	457	6.7	308	8000	4		1/4	0/4
Her2/neu.952	10	YMIMVKCWM	4337	20	307	83	116	267	5		0/1	0/1
Her2/neu.5	9	ALCRWGGLL	4338	100	-- ²	278	--	--	2		2/2	2/2
Her2/neu.5B3V9	9	ALBRWGGLV	4339	18	33	4.2	285	--	4	2/3	nt	0/3
Her2/neu.5M2V9	9	AMCRWGGLV	4340	179	7167	63	128	--	3	1/2	nt	0/2
Her2/neu.369		KIFGSLAFL	4341	36.0	9	19	23.0	3333	4	10/11		7/11
Her2/neu.369L2V9		KLFGSLAFV	4342	5.8	7.5	19	17.0	1269	4	4/4	3/4	2/4
Her2/neu.369V2V9		KVFGSLAFV	4343	20.0	19	769	15.0	29	4	4/4	3/4	2/4
Her2/neu.369T2V9		KTFGSLAFV	4344	35.0	13	1010	14.0	17	4	nt	nt	nt
Her2/neu.665		VVLGVVFGI	4345	14.0	--	2500	430.0	2000	2	see Table XXVII		
Her2/neu.665L2V9		VLLGVVFGV	4346	2.4	17	14	6.0	8000	4	4/4	2/4	0/4
Her2/neu.952	10	YMIMVKCWM	4347	20	307	83	116	267	5		0/1	0/1
Her2/neu.952L2B7V10	10	YLMVKCBWMV	4348	7.2	66	77	11	851	4	3/3	nt	0/3

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

added

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays					Radiolabeled peptide	
Species	Antigen	Allele	Cell line	Source	Sequence	SEQ ID NO:
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	4349
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFSPV	4350
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFSPV	4351
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFSPV	4352
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFSPV	4353
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFSPV	4354
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK	4355
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	4356
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF	4357
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	4358
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	4359
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	STLPETYVVR	4360
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	4361
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLVL	4362
	B8	B*0801	Steinlin	HIV gp 586-593 Y1->F, Q5->Y	FLKDYQLL	4363
	B27	B*2705	LG2	R 60s	FRYNGLIHR	4364
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	FPFKYAAAF	4365
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF	4366
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF	4367
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	4368
	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF	4369
	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF	4370
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF	4371
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL	4372
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	4373
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	4374
Mouse	D ^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	4375
	K ^b		EL4	VSV NP 52-59	RGYVVFQGL	4376
	D ^a		P815	HIV-IIIIB ENV G4->Y	RGPYRAFTI	4377
	K ^a		P815	non-natural (KdCON1)	KFNPMKTYI	4378
	L ^a		P815	HBVs 28-39	IPQSLDSYWTSL	4379

B. Class II binding assays

Radiolabeled peptide

Species	Antigen	Allele	Cell line	Source	Sequence	SEQ ID NO:
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVVKQNTLKLAT	4380
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIIVTPRTPPY	4381
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAAAF	4382
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIADFDEEAR	4383
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT	4384
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA	4385
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT	4386
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT	4387
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE	4388
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE	4389
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE	4390
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE	4391
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE	4392
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALHQLKINPYVLS	4393
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE	4394
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE	4395
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVVKQNTLKLAT	4396
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL	4397
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT	4398
	DQ3.1	QA1*0301/DQB1*0301	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	4399
Mouse	IA ^b		DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	4400
	IA ^d		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	4401
	IA ^k		CH-12	HEL 46-61	YNTDGGSTDYGILQINSR	4402
	IA ^s		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	4403
	IA ^u		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	4404
	IE ^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK	4405
	IE ^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK	4406

added

Table XXVI. Crossbinding data of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
Her2/neu.5	9	ALCRWGLL	4407	100	--	278	--	--	2
Her2/neu.5	10	ALCRWGLLA	4408	139	1955	12	1947	2500	2
Her2/neu.48	9	HL YQGCQVV	4409	139	307	13	514	1143	3
Her2/neu.106	9	QLFEDNYAL	4410	17	226	11	463	2105	4
Her2/neu.106	10	QLFEDNYALA	4411	357	662	9.1	218	74	4
Her2/neu.144	10	SLTEILKGGV	4412	238	--	22	--	--	2
Her2/neu.153	9	VLIQRNPQL	4413	23	3909	3.3	1057	--	2
Her2/neu.369	9	KIFGSLAFL	4414	36	9.0	19	23	3333	4
Her2/neu.435	9	ILHNGAYSL	4415	75	358	100	569	--	3
Her2/neu.466	9	ALJHNTHL	4416	278	1265	10	1762	--	2
Her2/neu.508	9	GLACHQLCA	4417	417	--	127	--	9091	2
Her2/neu.653	9	SIISAVVGI	4418	69	524	35	285	148	4
Her2/neu.665	9	VVLGVVFGI	4419	14	--	2500	430	2000	2
Her2/neu.689	9	RLIQETELV	4420	21	--	625	34	--	2
Her2/neu.767	9	ILDEAYVMA	4421	238	--	4167	3083	--	1
Her2/neu.773	10	VMAGVGSPYV	4422	200	391	13	3700	--	3
Her2/neu.789	9	CLTSTVQLV	4423	208	457	6.7	308	8000	4
Her2/neu.799	9	QLMPYGCCL	4424	217	977	114	712	--	2
Her2/neu.952	10	YMIMVKCWM	4425	20	307	83	116	267	5
Her2/neu.952	9	YMIMVKCWM	4426	217	--	625	2643	1000	1

-- indicates binding affinity = 10,000nM.

added

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Wild-type ¹	CTL Tumor ¹	CTL Wild-type ²	CTL Tumor ²
Her2/neu.5	9	ALCRWGILL	4427	100	-- ³	278	--	--	2	2/2	2/2	2/2	1/2
Her2/neu.48	9	HL YQGQVV	4428	139	307	13	514	1143	3	1/2	0/2	2/2	1/2
Her2/neu.106	9	QLFEDNYAL	4429	17	226	11	463	2105	4	0/2	0/2		
Her2/neu.106	10	QLFEDNYALA	4430	357	662	9.1	218	74	4	0/2	0/2		
Her2/neu.369	9	KIFGSLAFL	4431	36	9.0	19	23	3333	4	6/7	4/7	2/2	2/2
Her2/neu.435	9	ILHNGAYSL	4432	75	358	100	569	--	3	3/3	1/3	2/2	2/2
Her2/neu.653	9	SIISAVVGI	4433	69	524	35	285	148	4	0/3		2/2	2/2
Her2/neu.665	9	VVLGVVFGI	4434	14	--	2500	430	2000	2			2/2	1/2
Her2/neu.773	10	VMAGVGSPYV	4435	200	391	13	3700	--	3	1/2	0/2	1/2	1/2
Her2/neu.789	9	CLTSTVQLV	4436	208	457	6.7	308	8000	4	1/4	0/4	1/2	1/2
Her2/neu.952	10	YMIMVKCWM	4437	20	307	83	116	267	5	0/1	0/1	2/2	2/2

1) Number of donors yielding a positive response/total tested.

2) Data from ovarian cancer patients.

3) -- indicates binding affinity = 10,000nM.

added

Table XXVIII. Immunogenicity A2 supermotif analog peptides

Source	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Crossbound	CTL Peptide ¹	CTL Wild-type ¹	CTL Tumor ¹
Her2/neu.5	ALCRWGLLL	4438	100	-- ²	278	--	--	2		2/2	2/2
Her2/neu.5B3V9	ALBRWGLLV	4439	18	33	4.2	285	--	4	2/3	nt	0/3
Her2/neu.5M2V9	AMCRWGLLV	4440	179	7167	63	128	--	3	1/2	nt	0/2
Her2/neu.369	KIFGSLAFL	4441	36.0	9	19	23.0	3333	4	10/11		7/11
Her2/neu.369L2V9	KLFGSLAFV	4442	5.8	7.5	19	17.0	1269	4	4/4	3/4	2/4
Her2/neu.369V2V9	KVFGSLAFV	4443	20.0	19	769	15.0	29	4	4/4	3/4	2/4
Her2/neu.369T2V9	KTFGSLAFV	4444	35.0	13	1010	14.0	17	4	nt	nt	nt
Her2/neu.665	VVLGVVFGI	4445	14.0	--	2500	430.0	2000	2			
Her2/neu.665L2V9	VLLGVVFGV	4446	2.4	17	14	6.0	8000	4	4/4	2/4	0/4
Her2/neu.952	YMIMVKCWMV	4447	20	307	83	116	267	5		0/1	0/1
Her2/neu.952L2B7V10	YLIMVKBWMV	4448	7.2	66	77	11	851	4	3/3	nt	0/3

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

added

Table XXIX. Her2/neu DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0241	2	LCRWGLLLALLPPGA	4449	Her2/neu.6	53	--	--	1
39.0242	2	RWGLLLALLPPGAAS	4450	Her2/neu.8	0.42	161	--	2
39.0243	2	WGGLLLALLPPGAAS	4451	Her2/neu.9	0.98	35	--	2
39.0244	2	GTDMKLRLPASPETH	4452	Her2/neu.28	5000	--	--	0
39.0245	2	DMKLRLPASPETHLD	4453	Her2/neu.30	5000	--	--	0
39.0246	2	NLELYLPTNASLSF	4454	Her2/neu.59	11	118	368	3
39.0247	3	LTYLPTNASLSFLQD	4455	Her2/neu.62	10	136	78	3
39.0248	2	TQLFEDNYALAVLDN	4456	Her2/neu.105	94	--	1563	1
39.0249	2	VCPLHNQEVTAEDGT	4457	Her2/neu.314	--	--	--	0
39.0250	2	CKKIFGSLAFLPESF	4458	Her2/neu.367	21	--	926	2
39.0251	2	LSVFQNLQVIRGRIL	4459	Her2/neu.422	28	672	86	3
39.0252	2	LRELGSGLALIHNT	4460	Her2/neu.458	161	--	--	1
39.0253	3	KPDLSYMPIWKFPDE	4461	Her2/neu.605	152	--	8621	1
39.0254	3	ASPLTSIISAVVGIL	4462	Her2/neu.648	56	--	714	2
39.0255	2	LTSIISAVVGILLVV	4463	Her2/neu.651	26	--	5102	1
39.0256	3	VVGILLVVVLGVVFG	4464	Her2/neu.658	--	--	--	0
39.0257	3	LLVVVLGVVFGILIK	4465	Her2/neu.662	>6250	--	--	0
39.0258	2	VLGVVFGILIKRRQQ	4466	Her2/neu.666	71	--	781	2
39.0259	2	ETELVEPLTPSGAMP	4467	Her2/neu.693	833	--	--	1
39.0260	2	VEPLTPSGAMPNQAQ	4468	Her2/neu.697	>6250	--	--	0
39.0261	2	ETELRKVKVLGSGAF	4469	Her2/neu.717	313	1286	658	2
39.0262	2	GENVKIPVAIKVLRE	4470	Her2/neu.743	79	--	807	2
39.0263	2	IKVLRENTSPKANKE	4471	Her2/neu.752	--	--	--	0
39.0264	3	KEILDEAYVMAGVGS	4472	Her2/neu.765	--	6164	--	0
39.0265	3	DEAYVMAGVGSPPYVS	4473	Her2/neu.769	100	196	125	3
39.0266	2	SRLLGICLTSTVQLV	4474	Her2/neu.783	14	375	45	3
39.0267	2	TVQLVTQLMPYGCLL	4475	Her2/neu.793	22	978	2500	2
39.0268	3	LLNWCMQIAKGMSYL	4476	Her2/neu.822	6.0	--	208	2
39.0269	2	ITDFGLARLLDIDET	4477	Her2/neu.861	1042	--	--	0
39.0270	3	KVPIKWMALESILRR	4478	Her2/neu.883	2.3	652	1316	2
39.0271	3	PIKWMALESILRRRF	4479	Her2/neu.885	6.3	1286	3205	1
39.0272	2	IKWMALESILRRRFT	4480	Her2/neu.886	5.3	1125	6250	1
39.0273	2	GVTWELMTFGAKPY	4481	Her2/neu.909	3.6	1364	1471	1
39.0274	3	VWELMTFGAKPYDGI	4482	Her2/neu.912	58	818	676	3
39.0275	2	GERLPQPICTIDVY	4483	Her2/neu.938	--	--	--	0
39.0276	2	QPICTIDVYMIMVK	4484	Her2/neu.943	75	7500	250	2
39.0277	2	DVYMIMVKCWMIDSE	4485	Her2/neu.950	179	790	192	3
39.0278	2	QGFFCPDPAPGAGGM	4486	Her2/neu.1028	--	1957	--	0
39.0279	3	TDGYVAPLTCSPQPE	4487	Her2/neu.1124	--	--	--	0
39.0280	2	QPDVRPQPPSPREGP	4488	Her2/neu.1142	7143	--	--	0
39.0281	2	PSTFKGTPTAENPEY	4489	Her2/neu.1234	--	--	--	0

-- indicates binding affinity = 10,000nM.

↑
added

Table XXX. DR supertype crossbinding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2B1 nM	DR2w2B2 nM	DR6w19 nM	DR5w11 nM	DR8w2 nM	DR147 Binding	Broad Binding (5/8)
39.0242	RWGLLLALLPPGAAS	4490	Her2/neu.8	0.40	161	--	70	741	--	282	408	2	6
39.0243	WGLLLALLPPGAAS	4491	Her2/neu.9	1.0	35	--	43	1818	--	80	109	2	5
39.0246	NLELTYPNTASLSF	4492	Her2/neu.59	11	118	368	325	2222	2059	4000	2227	3	4
39.0247	LTYLPTNASLSFLQD	4493	Her2/neu.62	10	136	78	910	357	125	4878	9074	3	6
39.0250	CKKIFGSLAFLPESF	4494	Her2/neu.367	21	--	926	1300	--	1029	--	--	2	2
39.0251	LSVFQNLQVIRGRIL	4495	Her2/neu.422	28	672	86	325	270	614	2000	1485	3	6
39.0254	ASPLTSIISAVVGIL	4496	Her2/neu.648	56	--	714	96	5405	73	--	--	2	4
39.0258	VLGVVFGILKRRQQ	4497	Her2/neu.666	71	--	781	827	323	233	43	77	2	7
39.0261	ETELRKVKVLGSGAF	4498	Her2/neu.717	313	1286	658	4790	3846	2500	3279	1960	2	2
39.0262	GENVKIPVAIKVLR	4499	Her2/neu.743	79	--	807	1936	5882	8750	--	--	2	2
39.0265	DEAYVMAGVGSPYVS	4500	Her2/neu.769	100	196	125	3138	833	1750	7407	860	3	5
39.0266	SRLLGICLTSTVQLV	4501	Her2/neu.783	14	375	45	414	--	10	1429	--	3	5
39.0267	TVQLVTQLMPYGCLL	4502	Her2/neu.793	22	978	2500	12	--	1129	--	7101	2	3
39.0268	LLNWCMMQIAKGMSYL	4503	Her2/neu.822	6.0	--	208	1597	17	90	50	120	2	6
39.0270	KVPIKWMALESILRR	4504	Her2/neu.883	2.3	652	1316	3.4	9.5	1129	2740	6203	2	4
39.0274	VWELMTFGAKPYDGI	4505	Her2/neu.912	58	818	676	92	200	8750	3704	5506	3	5
39.0276	QPPICTIDVYMIMVK	4506	Her2/neu.943	75	7500	250	169	7407	2692	4348	9608	2	3
39.0277	DVYMIMVKCWMIDSE	4507	Her2/neu.950	179	790	192	1936	4762	--	909	1089	3	4

-- indicates binding affinity = 10,000nM.

added

Table XXXI. DR3 binding

Peptide	Sequence	SEQ ID NO:	Source	DR3 nM
39.0338	RLPASPETHLDMLRH	4508	Her2/neu.34	--
39.0339	SLSFLQDIQEVQGYV	4509	Her2/neu.70	5769
39.0340	VLIAHNQVRQVPLQR	4510	Her2/neu.84	--
39.0341	GTQLFEDNYALAVLD	4511	Her2/neu.104	1364
39.0342	DTILWKDIFHKNNQL	4512	Her2/neu.165	--
39.0343	ALTLDITNRSRACHP	4513	Her2/neu.180	8571
39.0344	KGPLPTDCCHEQCAA	4514	Her2/neu.228	--
39.0345	LVTYNTDTFESMPNP	4515	Her2/neu.271	--
39.0346	YNYLSTDVGSC TLVC	4516	Her2/neu.301	--
39.0347	NQEVTAEDGTQRCEK	4517	Her2/neu.319	--
39.0348	CYGLGMEHLREVRV	4518	Her2/neu.342	--
39.0349	SLAFLPESFDGDPAS	4519	Her2/neu.373	--
39.0350	PESFDGDPASNTAPL	4520	Her2/neu.378	--
39.0351	TAPLQPEQLQVFETL	4521	Her2/neu.389	--
39.0352	LALIHNTLHLCFVHT	4522	Her2/neu.465	968
39.0353	VHTVPWDQLFRNPHQ	4523	Her2/neu.477	--
39.0354	WDQLFRNPHQALLHT	4524	Her2/neu.482	333
39.0355	LQGLPREYVNARHCL	4525	Her2/neu.547	--
39.0356	VTCFGPEADQCVACA	4526	Her2/neu.574	--
39.0357	PSGVKPDLSYMPIWK	4527	Her2/neu.601	--
39.0358	IWKFPDEEGACQPCP	4528	Her2/neu.613	--
39.0359	HSCVDLDDKGCPAEQ	4529	Her2/neu.632	--
39.0360	MRRLQETELVEPLT	4530	Her2/neu.687	--
39.0361	QMRILKETELRKVKV	4531	Her2/neu.711	938
39.0362	AIKVLRENTSPKANK	4532	Her2/neu.751	--
39.0363	NKEILDEAYVMAGVG	4533	Her2/neu.764	--
39.0364	GMSYLEDVRLVHRDL	4534	Her2/neu.832	1667
39.0365	VRLVHRDLAARNVLV	4535	Her2/neu.839	882
39.0366	ARLLDIDETEHADG	4536	Her2/neu.867	968
39.0367	ETEHADGGKVPIKW	4537	Her2/neu.874	--
39.0368	IKWMALESILRRRFT	4538	Her2/neu.886	682
39.0369	CWMIDSECRPRFREL	4539	Her2/neu.958	667
39.0370	FRELVSEFSRMARDP	4540	Her2/neu.969	4225
39.0371	FSRMARDPQRFVVIQ	4541	Her2/neu.976	1875
39.0372	FVVIQNEDLGPASPL	4542	Her2/neu.986	--
39.0373	YRSLEDDDMGDLVD	4543	Her2/neu.1005	4762
39.0374	RSLEDDDMGDLVDA	4544	Her2/neu.1006	--
39.0375	GDLVDAEEYLPQQG	4545	Her2/neu.1015	--
39.0376	QGFFCPDPAPGAGGM	4546	Her2/neu.1028	--
39.0377	DLTLGLEPSEEEAPR	4547	Her2/neu.1058	--
39.0378	SDVFDGDLGMGAAG	4548	Her2/neu.1083	--
39.0379	LQRYSEDPTVPLPSE	4549	Her2/neu.1109	--
39.0380	TVPLPSETDGYVAPL	4550	Her2/neu.1117	--
39.0381	KNGVVKDVFAFGGAV	4551	Her2/neu.1177	--
39.0382	QGGAAPQPHPPAFS	4552	Her2/neu.1200	--
39.0383	DNLYYWDQDPPERGA	4553	Her2/neu.1218	--

-- indicates binding affinity = 10,000nM.

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added

Table XXXII. HTL candidates

Peptide	Sequence	SEQ ID NO.	Motif	Source	DR1 nM	DR4w 4 nM	DR7 nM	DR3 nM	DR2w2B 1 nM	DR2w2B 2 nM	DR6w19 nM	DR5w11 nM	DR8w2 nM	DR147 Degen (5/8)	Broad Degen Binder
39.0242	RWGLLALLPPGAAS	4554	DR sup	Her2/neu.8	0.40	161	--	--	70	741	--	282	408	2	6
39.0243	WGGLLALLPPGAAS	4555	DR sup	Her2/neu.9	1.0	35	--	--	43	1818	--	80	109	2	5
39.0247	LTYLPTNASLSFLQD	4556	DR sup	Her2/neu.62	10	136	78	--	910	357	125	4878	9074	3	6
39.0251	LSVFQNLQVIRGRIL	4557	DR sup	Her2/neu.422	28	672	86	--	325	270	614	2000	1485	3	6
39.0352	LALIHNTHLFCVHT	4558	DR3	Her2/neu.465	357	>8182	1250	968	92	--	4.7	8000	1485	1	3
39.0354	WDQLFRNPHQALLHT	4559	DR3	Her2/neu.482	--	>8182	--	333	6067	--	85	--	--	0	1
39.0258	VLGVVFGILKRRQQ	4560	DR sup	Her2/neu.666	71	--	781	--	827	323	233	43	77	2	7
39.0361	QMRILKETELRKVKV	4561	DR3	Her2/neu.711	119	>8182	1923	938	607	34	4375	4878	7656	1	3
39.0265	DEAYVMAGVGSPYVS	4562	DR sup	Her2/neu.769	100	196	125	--	3138	833	1750	7407	860	3	5
39.0266	SRLGICLTSTVQLV	4563	DR sup	Her2/neu.783	14	375	45	--	414	--	10	1429	--	3	5
39.0268	LLNWCMQIAKGMSYL	4564	DR sup	Her2/neu.822	6.0	--	208	--	1597	17	90	50	120	2	6
39.0365	VRLVHRDLAARNVLV	4565	DR3	Her2/neu.839	147	3058	1087	882	1422	6061	81	74	490	1	4
39.0366	ARLLDIDETEHADG	4566	DR3	Her2/neu.867	--	>8182	--	968	--	--	--	--	--	0	0
39.0270	KVPIKWMALLESILRR	4567	DR sup	Her2/neu.883	2.3	652	1316	4839	3.4	9.5	1129	2740	6203	2	4
39.0368	IKWMALESILRRFT	4568	DR3	Her2/neu.886	17	3224	4098	682	11	2.5	2500	370	731	1	5
39.0274	VWELMTFGAKPYDGI	4569	DR sup	Her2/neu.912	58	818	676	--	92	200	8750	3704	5506	3	5
39.0369	CWMIDSECRPRFREL	4570	DR3	Her2/neu.958	1389	>8182	--	667	--	1333	--	--	--	0	0

-- indicates binding affinity = 10,000nM.

a d d e c l